us-09-936-956-1.rag

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(AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                   Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-663416/62.
N-PSDB; ADE44813.
                                                                                                                                                                                                                                                                               WO2003063766-A2.
                                                                                                                                                                                                                                                                                                                                                        Zlotnick GW,
                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                                                                                                              07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                Metcalf BJ
                                                                                                                                                                                          ADE44814;
                                                                                                                                                                       ADE44814
                                                                                                                                                                                    Neisseria
                                                                                                                                                                                                                                                                                                                                                                                     Human HLA
                                                                                                                                                                                                                                                                                                                                                                                          Breast ca
                                                                                                                                                                                                                                                                                                                                                                                                  Human CEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEA antig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human car
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                                                                                                                                                                                                                                                                                                                                                                             Caulobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-A24
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                                                                                                                                                                                                                                                                                                                                                                                                               HLA-A24
                                              (without alignments)
184.386 Million cell updates/sec
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                                      February 24, 2005, 15:03:10 ; Search time 117.463 Seconds
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                                                                                                                                                                                                                                                                                                           Description
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Adf83690 1
Adg38740 1
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Add23187
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Aaw37490
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Aay00835
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                               2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                          OM protein - protein search, using sw model
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AAY46550
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
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                                                                                                                                          seq length: 0
seq length: 200000000
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98
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274
1026
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Match
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Perfect
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_	Aao24401 HLA-A24-r	Adm12345 MHC class	Ado38565 Carcinoem	Adp80010 Human HLA		Abull918 Human HGP		Aab88018 CD66 pept	Aab88099 CD66 pept	CD66	Abp67248 Human CD6	Abull935 Human HGP	Abul1953 Human HGP	Abull944 Human HGP	Abull956 Human HGP	Abp83373 G protein		Aau89150 Insulin/i	Ada03975 IGF-1R re
ADG38664	AA024401	ADM12345	ADO38565	ADP80010	AAR67090	ABU11918	AAB88073	AAB88018	AAB88099	AAB88056	ABP67248	ABU11935	ABU11953	ABU11944	ABU11956	ABP83373	ABM74254	AAU89150	ADA03975
7	œ	œ	æ	8	~	9	4	4	4	4	Ŋ	9	9	ø	9	9	7	ß	9
10	10	10	10	10	12	12	14	14	14	14	14	14	14	15	15	15	15	18	18
23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5
23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	53	23
56	27	28	29	30	31	32	33		35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ORF2086; Neisseria meningitidis serogroup B infection; antibacterial; antiinflammatory; immune response; bacterial meningitis; Streptococcus pneumoniae infection; non-pathogenic; immunogenic composition; 2086 protein. Neisseria meningitidis ORF2086 protein SeqID248. ADE44814 standard; protein; 260 AA. (first entry)

11-OCT-2002; 2002WO-US032369

11-OCT-2001; 2001US-0328101P. 30-AUG-2002; 2002US-0406934P.

Farley J, Bernfield LA, Zagursky RJ; . E Fletcher

Composition comprising crossreactive immunogenic antigen encoded by open reading frame 2086 of Neisseria sp., that provides immunogenicity against meningitis, or its immunogenic portion or biological equivalent.

Claim 60; SEQ ID NO 248; 480pp; English

This invention relates to a novel composition which comprises at least one protein (or fragment of) encoded by an open reading frame (ORF) of a Neisseria sp. (ORF2086), where the ORF encoding a crossreactive immunogenic antigen provides immunogenicity against infection by Neisseria meningitidis serogroup B in a subject. The composition of the invention may have antibacterial or antiinflammatory activity through the induction of the immune response. The invention may be useful for the treatment of bacterial meningitis in a mammal. One or more polypeptides

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising crossreactive immunogenic antigen encoded by open reading frame 2086 of Neisseria sp., that provides immunogenicity against meningitis, or its immunogenic portion or biological equivalent.
or nucleic acids encoding such polypeptides are useful in a composition or as a part of the treatment regimen for the prevention of amelioration of Streptococcus pneumoniae infection. The composition of the invention is non-pathogenic and substantially free from any infectious impurities. The immunogenic compositions can be compounded with fewer components to selicit protection compazable to previously used agents. The present sequence is the amino acid sequence of a Neisseria meningitidis strainspecific mature 2086 protein with a native leader sequence which can be used to create the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORF2086; Neisseria meningitidis serogroup B infection; antibacterial; antiinflammatory; immune response; bacterial meningitis; Streptococcus pneumoniae infection; non-pathogenic; immunogenic composition; 2086 protein.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
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                                                                                                                                                                                                                                                        Query Match 25.5%; Score 25; DB 7; Length 260; Best Local Similarity 25.0%; Pred. No. 1.5e+03; Matches 6; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis ORF2086 protein SeqID252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 60; SEQ ID NO 252; 480pp; English.
                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                    NGTLTLSAQGAEKTYGNGDSLNTG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE44818 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                          33 NGTFXXXXXXXXXXGDXXXXG
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2002US-0406934P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-663416/62.
                                                                                                                                                                                                                   Sequence 260 AA;
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Metcalf BJ;
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30-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE4481U
ID ADI
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This invention relates to a novel composition which comprises at least one protein (or fragment of) encoded by an open reading frame (ORF) of a Neisseria sp. (ORF2086), where the ORF encoding a crossreactive immunogenic antigen provides immunogenicity against infection by Neisseria meningitidis serogroup B in a subject. The composition of the immune response. The invention may bave antibacterial or antiinflammatory activity through the induction of the immune response. The invention may be useful for the treatment of bacterial meningitis in a mammal. One or more polypeptides or nucleic acids encoding such polypeptides are useful in a composition of ras a part of the treatment regimen for the prevention of amelioration of Streptococcus pneumoniae infection. The composition of the invention is non-pathogenic and substantially free from any infectious impurities. The immunogenic compositions can be compounded with fewer components to elicit protection comparable to previously used agents. The present sequence is the amino acid sequence of a Neisseria meningitidis strain-
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition comprising crossreactive immunogenic antigen encoded by open reading frame 2086 of Neisseria sp., that provides immunogenicity against meningitis, or its immunogenic portion or biological equivalent.
The immunogenic compositions can be compounded with fewer components to elicit protection comparable to previously used agents. The present sequence is the amino acid sequence of a Neisseria meningitidis strainspecific mature 2086 protein which can be used to create the composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial;
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
                                                                                                                                                                                                                ò
                                                                                                                                                                        Length 260;
                                                                                                                                                                                                                18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORF2086; Neisseria meningitidis serogroup B infection; ar
antilifammatory; immune response; bacterial meningitis;
Streptococcus pneumoniae infection; non-pathogenic;
immunogenic composition; 2086 protein; P4 leader.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis ORF2086 protein SeqID250.
                                                                                                                                                                      Query Match
25.5%; Score 25; DB 7; I
Best Local Similarity 25.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 60; SEQ ID NO 250; 480pp; English
                                                                                                                                                                                                                                                          33 NGTFXXXXXXXXXXXG 56
                                                                                                                                                                                                                                                                                               48 NĠTLTLSAQGAEKTYGNĠĎSLNTĠ 71
                                                                                                                                                                                                                                                                                                                                                                                                            ADE44816 standard; protein; 261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001; 2001US-0328101P. 30-AUG-2002; 2002US-0406934P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
Haemophilus influenzae.
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                                                                                      the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADE44815.
                                                                                                                              Sequence 260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003063766-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                               RESULT 3
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88888888
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Gaps

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18; Indels

Length 274;

Score 25; DB 8; I Pred. No. 1.6e+03; 0; Mismatches

25.5%;

Conservative

Query Match Best Local Similarity Local 6; Conserve

33 NGTFXXXXXXXXXXXG 56

85

NGTLTLSAQGAEKTYGNGDSLNTG

g

AAR48993 standard; protein; 1026 AA

RESULT 5 AAR48993 (first entry)

rsaA S-lyaer protein.

(revised)

16-OCT-2003 14-SEP-1994

AAR48993;

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The present invention relates to composition (1) comprising at least two multiple variants of meningococcal protein NMB1870 (ADP70202-ADP70246, ADP70280-ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70280-ADP70290 at antipody response effective against each of serogroup B Neisseria meningitidis strains MC59, 961-5945 and M1239, and also elicit an antibody response which is bactericidal against N. comingitidis strains in at least 2 of hypervirulent lineages ET-37, ET-5, cluster A4, lineage 3, subgroup I, subgroup II, and subgroup IV-1. In CCC MMB1870 is a lipoproterior. In (1) at least one of the proteins does not include the amino acid sequence ADP70271 or ADP70272 within 10 amino ccd sequences ADP70273 within 10 amino acid sequences ADP70273 within 10 amino acid sequence CC the amino acid sequences ADP70273 within 10 amino acid sequence CC at least one of the proteins includes the amino acid sequence CC ADP70274. ADP70274 are sequence motifs for retention or omission from the NMB1870 proteins. (1) or (11) is efficiently elicits systemic and/or mucosal immunity and thereby prevents/treat meningitis and cateraemia. (1) is useful as medicament and for raising an antibody includes the employed and proteins and passerial
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; Antiinflammatory; Vaccine; meningococcal protein; NMB1870; antigen; bactericide; meningitis; bacteraemia; Neisserial infection;
specific mature 2086 protein with a P4 leader sequence (derived from the Haemophilus influenzae P4 protein) which can be used to create the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for producing medicament for preventing Neisserial infection in mammal, comprising multiple variant of meningococcal protein NMB1870,
                                                                                                                                                                      Gaps
                                                                                                                                                                      ö
                                                                                                                      25.5%; Score 25; DB 7; Length 261; 25.0%; Pred. No. 1.5e+03; ive 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis NMB1870 protein, SEQ ID 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis; strain ISS1113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 128; 77pp; English.
                                                                                                                                                                                                         33 NGTFXXXXXXXXXXXG 56
                                                                                                                                                                                                                                                 49 NGTLTLSAQGAEKTYGNGDSLNTG 72
                                                                                                                                                                                                                                                                                                                                                            ADP70329 standard; protein; 274 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2002; 2002GB-00027346
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comanducci M, Pizza M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-468293/44.
                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON SRL.
                                                                                 Sequence 261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004048404-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                      ADP70329;
                                                                                                                          Query Match
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C. crescentus; rsaA; paracrystalline; S-layer; protein; heterologous; cellulase; xylase; metallothionein; restriction site; reading frame; fusion protein; bioreactor; toxic metal; sewage; waste water; wood pulp suspension; cell surface; vaccine; fish.

Caulobacter vibrioides

(UYBR-) UNIV BRITISH COLUMBIA.

WPI; 1994-066249/09. Smit J, Bingle WH;

N-PSDB; AAQ57972

93CA-02090549. 92US-00895367.

26-FEB-1993; 09-JUN-1992;

10-DEC-1993.

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This sequence is encoded by the C. crescentus rsaA gene and represents the paracrystalline S-layer protein. The rsaA gene was used in the production of the heterologous protein of the invention. The heterologous protein is produced by cloning a polypeptide coding sequence, estimated by cloning the fusion sequence in Caulobacter. This S- layer protein bacterial system can be used in bioreactors, est to bind toxic metals in sewage waste can be used in bioreactors, est to bind toxic metals in sewage waste be used to produce heterologous proteins at the cell surface for use in vaccines, partic. fish vaccines proteins at the cell surface in synthesised in large quantities and has a general repetitive sequence, permitting the synthesise of large amounts of heterologous protein as a fusion product and presentation at the cell surface. (Updated on 16-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodn. of heterologous polypeptides in bacteria, partic. Caulobacter - by expression of a fusion prod. of the polypeptide sequence and a bacterial S-layer protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Fig 6; 27pp; English.
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1026 AA;
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8
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Sequence 274 AA;

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Caulobacter crescentus S-layer rsaA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-470880/43.
N-PSDB; AAV01866.
                                                                                                                                                                                                                                                                                                                                                        Smit J, Bingle WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1026 AA;
                                                                               wood pulping.
                                                                                                                                                          WO9734000-A1.
                                                                                                                                                                                                                                    10-MAR-1997;
                                                                                                                                                                                                                                                                           12-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2003
04-MAY-2000
                                                                                                                                                                                              18-SEP-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Caulobacter crescentus CB15 paracrystalline S-layer protein (AAR17717) is encoded by the reaA gene (AAR17717). It can be used as a fusion partner with polypeptides of interest, allowing presentation of the polypeptide on the surface of the Caulobacter cells. The bacterium is cultured as a biofilm in a bioreactor or may be used to present an artigenic epitope (see ARR94016 and AAR94018) to the environment e.g. for use as a vaccine. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression and presentation of polypeptide heterologous to Caulobacter S-layer protein to bacterium's environment - by cloning in-frame into Caulobacter reak gene, and expressing as fusion prod. with S-layer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                        860. .905
/note= "glycine-aspartic acid repeat region"
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                                                                                                                                                                                                                                                                     S-layer; rsaA gene; surface protein; biofilm; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 NDTFVAGEVAGAATLTVGDTLSGG 290
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                                                                          AAR94014 standard; protein; 1026 AA.
                                                                                                                                                                                                                                                                                                             Caulobacter vibrioides; strain CB15.
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-00895367.
                                                                                                                                                                                                                                Caulobacter S-layer protein.
                                                                                                                                                     (revised)
(revised)
(first entry)
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Best Local Similarity 25.00,
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(first entry)
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N-PSDB; AAT17717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bingle WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1026 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1992;
                                                                                                                                                                                            21-MAY-1996
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20-APR-1998
                                                                                                                                                     16-OCT-2003
25-MAR-2003
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                                                                                                                 AAR94014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smit J,
                                                                                                                                                                                                                                                                                                                                                                          Region
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ID AAW:
XX
AC AAW
XX
DT 17--
DT 20--
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                                    RESULT 6
                                                        AAR9401
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                                                                          SO CCC CCC X S X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B
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The present sequence represents a Caulobacter S-layer protein used in an example of the present invention. A new DNA construct has been developed which contains at least one restriction site for insertion of DNA upstream of DNA encoding a C-terminal region of at least the last 82 amino acids (aa) of Caulobacter S-layer protein. Caulobacter containing the DNA constructs above additionally containing a sequence encoding a heterologous polypeptide, are particularly useful in live vaccines (where the DNA constructs above additionally containing a sequence encoding a heterologous polypeptide is an antigen). They can also be used for production of e.g. ligands, enzymes or other proteins, e.g. production of e.g. ligands, enzymes or other proteins, e.g. metallothionalins to remove heavy metals from water or sewage, or xylanase or callulase for use in wood pulping All known Caulobacter strains are harmless, and stable in outdoor environments, including water (so suitable for waccinating fish) or soil. They are well suited for growing in biofilm reactors and produce S-layer proteins, which is an ideal system for presentation of antigens, at high level. (Updated on 17-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA containing sequence for C-terminal region of Caulobacter S-layer protein - expressed as fusion proteins containing antigenic peptides in Caulobacter, useful as live vaccines.
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S-layer; rsaA gene; Caulobacter; vaccine; antigenic; ligand; enzyme; metallothionein; heavy metal; water; sewage; xylanase; cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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25.0%; Pred. No. 6.2e+03;
iive 0; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nomellini JF;
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Query Match
Best Local Similarity 25.0%,
Best Local 6; Conservative
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                                                                                                                                                                         Caulobacter vibrioides.
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Bingle WH;

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The present invention relates to Caulobacter deficient in a protease native to Caulobacter that cleaves hybrid Caulobacter S-layer protein monomers. The Caulobacter is useful as a host cell for expression of a hybrid Caulobacter S-layer protein monomer or for the expression of heterologous peptides. The Caulobacter is also useful as an expression system for producing random libraries of peptides or gene fragments for display and panning purposes. This system is useful for the expression of unknown or uncharacterised peptides. The present sequence is Caulobacter crescentus RsaA protein. (Updated on 23-OCT-2001 to standardise OS field)
                                                                                                                                                                                                                                                         New Caulobacter deficient in a protease native to Caulobacter that cleaves hybrid Caulobacter S-layer protein monomers, useful as a host cell for expressing a hybrid S-layer protein monomer, or for expressing
                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 8; 49pp; English.
                                                                                                                                      (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                22-MAY-2001; 2001CA-02347657.
                                                         22-MAY-2002; 2002WO-CA000722
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Best Local Similarity 25.v.
6; Conservative
                                                                                                                                                                               Smit J, Nomellini JF,
                                                                                                                                                                                                                                                                                                                       heterologous peptides
                                                                                                                                                                                                                       WPI; 2003-148470/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-2004
              28-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a method for cleaving a recombinant fusion protein which is produced by Caulobacter and consists of Caulobacter surface layer (S-layer) protein (containing the C-terminal secretion signal) and a target protein heterologous to Caulobacter. The cleavage of target protein from the S-layer protein is carried out under mild acid conditions so that cleavage occurs at aspartate proline dipptide site without solubilising the protein. The cleavage is accomplished while the fusion protein is in an insoluble aggregate form which facilitates protein. The method is useful for producing pure proteins including recombinant human and animal therapeutic antibiotic and vaccine peptides, enzymes, protein polymers, and antibacterial conzymes for foodstuffs. The present sequence is a S-layer protein from C: crescentus. The S-layer secretion signal, corresponding to the C-terminal portion of the protein from mino acid 690 onwards, is fused with a signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 target sequence for construction of a recombinant fusion construct which is expressed in Caulobacter. (Updated on 12-SEP-2003 to standardise OS
                                               /note= "Asp-Pro dipeptide present in S-layer secretion signal sequence. It is a site where a fusion protein comprising a target protein and the secretion signal is cleaved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage of Caulobacter produced recombinant fusion proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.5%; Score 25; DB 3; Length 1026; 25.0%; Pred. No. 6.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 21-23; 33pp; English
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              Location/Qualifiers
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                                                                                                                                                                                                                                           99WO-CA000637.
                                                                                                                                                                                                                                                                                   98CA-02237704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producing vaccine peptides
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                                                                                                                                                              WO200004170-A1
                                      Cleavage-site
                                                                                                                                                                                                                                           14-JUL-1999;
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14-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                  Smit J;
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DB 6; Length 1026;

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New HLA-Al, A2, A3, A24, B7 or B44 tumor associated antigen peptides, useful in preparing a composition for diagnosing or treating tumor associated antigen-related disease.
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44; tumour associated antigen peptide; cytostatic; vaccine; human.
                                                           18; Indels
25.5%; Score 25; DB 6; 1
25.0%; Pred. No. 6.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HLA-A24 epitope vaccine peptide SeqID266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sette A;
                                                           0; Mismatches
                                                                                                                                                                             267 NDTFVAGEVAGAATLTVGDTLSGG 290
                                                                                                                    33 NGTFXXXXXXXXXXXG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fikes JD,
                                                                                                                                                                                                                                                                                                                          ADP80011 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-2003; 2003WO-US038949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2002; 2002US-0432017P
                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keogh EA, Southwood S,
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                                         This invention relates to a novel isolated peptide which comprises at least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given in the specification. The peptide comprises HLA-A1, A2, A3, A34, B7 or B44 tumour associated antigen peptide. The invention may be useful for the production of compounds with a cytostatic activity or for the production of a vaccine. The peptide is useful in preparing a composition diagnosing or treating tumour associated antigen-related disease. The present sequence is that of an epitope peptide for use in the peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening, diagnosing and/or treating breast cancer by detecting a change in expression or activity of a breast cancer membrane protein (BCMP)
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast cancer; screening; diagnosis; breast cancer therapy; breast cancer membrane protein; BCMP; cytostatic; vaccine; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breast cancer membrane protein (BCMP) peptide SEQ ID NO:617.
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                Length 8;
                                                                                                                                                                                                                                            23.5%; Score 23; DB 8; Le
100.0%; Pred. No. 1.8e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide or encoding nucleic acid molecule.
               Claim 1; SEQ ID NO 266; 244pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terrett JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                ADD23187 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2003; 2003WO-GB001559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                            Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hudson LJ, Stamps AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-845381/78.
                                                                                                                                                                                                                                                                                                               NGTF 36
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                                                                                                                                                                                                                                                                                                                                    NGTF
                                                                                                                                                                                                               Sequence 8 AA;
                                                                                                                                                                               the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2004
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                comparing the expression or activity of the polypeptide or nucleic acid molecule, in the presence and absence of a candidate agent or in the presence of a control agent, and determining whether the candidate agent causes the expression or activity of the polypeptide or nucleic acid molecule to change; and (5) an agent identified by the method of (3) or activity of the polypeptide or causes the expression or activity of the polypeptide, or the expression of the nucleic acid molecule to change. BCMPs have cytostatic activities, and can be used in vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or their derivatives, are useful in the manufacture of a medicament for the treatment of breast cancer, where the composition is a vaccine. The present sequence represents a BCMP peptide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides and encoding nucleic acids that are useful epitopes of target-associated antigens, useful for diagnosing and/or treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
polypeptide or the nucleic acid molecule cited above, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 9;
1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   23.5%; Score 23; DB 100.0%; Pred. No. 1.8 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM72935 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CEA epitope SEQ ID NO:194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections, cancers and tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-2003; 2003WO-US027706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; tumour; human; CEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MANN-) MANNKIND CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-315564/29.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NGTF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004022709-A2
                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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Indels

1.5e+02; DB 2;

Length 10;

Query Match

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This sequence represents an HLA-A24 antigenic peptide sequence used in the cytotoxic T-lymphocytes (CTL) of the invention. The CTL recognise cells expressing on their surface a complex of an HLA-A24 molecule with an antigenic peptide. The antigenic peptide is an HLA-A24 restrained antigenic peptide. The CTLs can be used in the treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                      HLA-A24; antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex;
cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yasumoto M, Iwasaki T, Ideno M, Akiyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%; Score 23; DB 2; Le
100.0%; Pred. No. 1.5e+02;
cive 0; Mismatches 0;
             100.0%; Prec. ...
Score 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Page 70; 88pp; Japanese.
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                                                                                                                                                                                                                                   AAY00829 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-00203900.
97JP-00203917.
98JP-00014736.
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23.5%;
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Tanaka F, Kato I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                                                                      19-MAY-1999 (first entry)
                                     4; Conservative
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Best Local Similarity
Matches 4; Conserv
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -presenting cells.
                                                                                                         NGTF 10
                                                                                33 NGTF 36
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15-JUL-1997;
12-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic peptide having a human leukocyte antigen binding motif #1161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                         Gaps
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                                                                                                    0; Indels
                                                          23.5%; Score 23; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                  AAY46550 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US005039
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                                                                                Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immunisation
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                                                                                                                                              33 NGTF 36
                      Sequence 9 AA;
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Gaps

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Indels

(first entry)

19-MAY-1999

Sequence 10 AA;

AAY00830;

Length 10;

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(TAKI ) TAKARA SHUZO CO LTD.
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                                          WPI; 1999-132220/11
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                         33 NGTF 36
                                                                                                                                                                                                                                         7 NGTF 10
                                                                                                                                                                       Sequence 10 AA;
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15-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                    AAY00835;
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Matches
                                                                                                                                                                                                                                                                   RESULT 17
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                                                                                                                                                                                                                                                       This sequence represents an HLA-A24 antigenic peptide sequence used in the cytotoxic T-lymphocytes (CTL) of the invention. The CTL recognise cells expressing on their surface a complex of an HLA-A24 molecule with an antigenic peptide. The antigenic peptide is an HLA-A24 restrained antigenic peptide. The CTLs can be used in the treatment and diagnosis of
                                                                                                                                                                                                      Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen
               HLA-A24; antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex;
cancer; therapy; diagnosis.
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cancer; therapy; diagnosis.
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HLA-A24 antigenic peptide CE-203
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97JP-00203917.
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Fujie I, Tanaka F, Kato I;
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Best Local Similarity 100.v.
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                                                                                                                                            Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen -presenting cells.
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cancer; therapy; diagnosis.
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Akiyoshi
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   Ideno M,
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1.5e+02;
Iwasaki T,
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Yasumoto M,
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Takesako K, Nukaya I, Yasu
Fujie T, Tanaka F, Kato I;
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Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen-presenting cells.
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                                                                                                      HLA-A24; antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex; cancer; therapy; diagnosis.
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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                                                                              HLA-A24 antigenic peptide CE-204.
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Fujie T, Tanaka F, Kato I;
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Best Local Similarity 100.
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antigenic peptide. The CTLs can be used in the treatment and diagnosis of
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cancer; therapy; diagnosis.
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AAY00831
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Fujie I, Tanaka F, Kato I;
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Fujie T, Tanaka F, Kato I;
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                                                                                                                                                                      Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen -presenting cells.
                                                                                                                                                                                                                                                             This sequence represents an HLA-A24 antigenic peptide sequence used in the cytotoxic T-lymphocytes (CTL) of the invention. The CTL recognise cells expressing on their surface a complex of an HLA-A24 molecule with an antigenic peptide. The antigenic peptide is an HLA-A24 restrained antigenic peptide. The CTLs can be used in the treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen -presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-A24; antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex;
cancer; therapy; diagnosis.
                                                                                                    Akiyoshi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akiyoshi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                 Yasumoto M, Iwasaki T, Ideno M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ideno M,
                                                                                                                                                                                                                                                                                                                                                                                                 23.5%; Score 23; DB 2; Length 10;
100.0%; Pred. No. 1.5e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iwasaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yasumoto M,
                                                                                                                                                                                                                                    Example 9; Page 69; 88pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 77; 88pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY00834 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-A24 antigenic peptide CE-207.
          97JP-00203900.
97JP-00203917.
98JP-00014736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-00203900.
                                                                                               Takesako K, Nukaya I, Yasu<sup>.</sup>
Fujie T, Tanaka F, Kato I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TAKI ) TAKARA SHUZO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takesako K, Nukaya I, Yasu
Fujie I, Tanaka F, Kato I;
                                                                   (TAKI ) TAKARA SHUZO CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                            WPI; 1999-132220/11
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGTF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGTF 36
                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 AA;
          15-JUL-1997;
15-JUL-1997;
12-JAN-1998;
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15-JUL-1997;
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non-human transgenic mammal; HLA-A24; cytotoxic T cell; CTL; tumour; viral infection; antigen; chimeric; cytostatic; virucide; human.

HLA-A24 related human peptide, SEQ ID No 20.

(first entry)

26-FEB-2004

ADF83690;

ADF83690 standard; peptide; 10 AA.

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RESULT 24
                 4DF8369(
                                              The present invention relates to novel T-cell binding ligand (TCBL)

peptides (e.g. peptide G' (modified human MHC class II beta chain peptide

G, peptide J (human beta-2-microglobulin peptide) and HIV-1 peptides) and

TCBL peptide constructs for treating immunological disorders. The peptide

constructs are useful for eliciting a cellular immune response in a human

patient. The method comprises administering the peptide construct to the

petient preferably in combination with an immune response adjuvant. The

peptide constructs in the form of conjugated peptides are useful for

eliciting a cellular immune response in a patient exposed to or at risk

for exposure to the human immunodeficiency virus (HIV). The TCBL peptides

are useful for treating a patient suffering from an immunological

disorder such as herpes simplex virus (HSV) infection, malaria,

tuberculosis, cancers, acquired immunodeficiency syndrome (AIDS),

tuberculosis, cancers, acquired immunodeficiency syndrome (AIDS),

allergies, autoimmune myocarditis, diabetes and lupus) by

callergies (MS), autoimmune myocarditis, diabetes and lupus) by

antigenic peptide associated with the disorder. Unlike prior art peptide

conjugates, a modified version of peptide G has long range stabilisation

and also enhances the immune response. AAU82019-AAU82114 represent T-cell

peptide in the construct constructs or peptides used in
                                                                                                                                                               T-cell binding ligand; TCBL; peptide G'; human MHC class II beta chain; peptide J; human beta-2-microglobulin; HIV-1; TCBL peptide construct; immunological disorder; immune response; human immunodeficiency virus; herpes simplex virus infection; HSV; malaria; tuberculosis; cancer; CEA; acquired immunodeficiency syndrome; AIDS; allergy; autoimmune disease; autoimmune myocarditis; cytostatic; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New T cell binding ligand peptide for treating immunological disorders such as herpes simplex virus, tuberculosis, cancers, acquired immunodeficiency syndrome and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.5%; Score 23; DB 5; Length 10; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                     CEA antigenic peptide C3 associated with cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 27; 110pp; English.
                                             AAU82066 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                        24-MAY-2001; 2001WO-US016793.
                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2000; 2000US-0206548P.
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zimmerman DS, Sarin PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELS-) CEL-SCÌ CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-083037/11.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       their construction
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                                                                                                                                                                                                                                                                                                           WO200189286-A2.
                                                                                                                                                                                                                                                                                                                                          29-NOV-2001.
                                                                                                        09-APR-2002
                                                                                                                                                                                                                                                                              Synthetic.
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Non-human transgenic mammals expressing HLA-A24 with cytotoxic T cells induced by HLA-A24-restricted antigenic stimulation, useful in screening preventives or remedies for tumor or viral infections.

(SUMU) SUMITOMO PHARM CO LTD

WPI; 2003-067332/06.

Gotoh M;

12-DEC-2001; 2001WO-JP010885. 13-DEC-2000; 2000JP-00378556. 06-SEP-2001; 2001JP-00269746.

WO200247474-A1.

20-JUN-2002.

Homo sapiens.

Example 9; SEQ ID NO 20; 92pp; Japanese.

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The invention further relates to a novel non-human transgenic mammal transfected with an HLA-A24 gene in which cytotoxic T cells (CTL) are induced by HLA-A24-restricted antigenic stimulation. The invention further relates to a novel method of screening a remedy or a preventitive for a tumour or viral infection charaterised by comprising administering a test substance to the above-described non-human transgenic mammal and then assaying and evaluating whether or not CTLs specific to the test substance are induced therin. The invention also includes: a PSA-origin HLA-A24-restricted tumour antigen peptide selected by this screening method; a chimeric gene useful in forming the above-described transgenic con-human mammal, host cells transformed by this chimeric gene; and cutilisation thereof. The novel non-human transgenic mammal has cytostatic and virucide activity. This sequence represents a human HLA-A24 related peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%; Score 23; DB 7; Le 100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Matches 4; Conserv
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4; Conservative

Matches

NGTF 36 NGTF 10

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07-APR-2003; 2003WO-US010571.
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                                                                                                                                                                                                                                                                                                                    Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                 Producing analogs of Major Histocompatibility Complex (MHC) class I peptide epitopee, for treating viral diseases or cancer, comprise producing an analog having (semi)conservative amino acid substitutions of the MHC class I epitope.
                                                                                                                                                                                                                                                                                                      The invention comprises a method for producing a polypeptide that contains an analogue of a major histocompatability complex (MHC) class I peptide epitope, wherein the analogue has enhanced immunogenicity compared to the MHC class I peptide epitope. The method of the invention is useful for producing an analogue or heteroclitic analogue of an MHC class I peptide epitope analogue of an MHC class I peptide epitope analogues that can be used to treat viral diseases, cancer and other conditions characterized by displayed antigens on target cells. The present amino acid sequence prepresents a peptide of the invention which is derived from human conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major histocompatability complex class I epitope; MHC class I epitope; enhanced immunogenicity; heteroclitic analogue; immune response; viral disease; cancer; human; carcinoembryonic antigen.
major histocompatability complex class I epitope; MHC class I epitope; enhanced immunogenicity; heteroclitic analogue; immune response; viral disease; cancer; human; carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human carcinoembryonic antigen-derived peptide #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Preq. ...
                                                                                                                                                                                                                                                                                   Example 14; SEQ ID NO 178; 244pp; English.
                                                                                                                                                                                          Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG38664 standard; peptide; 10 AA
                                                                                                                                                                                           Tangri S,
                                                                                                                 07-APR-2003; 2003WO-US010571
                                                                                                                                       2002US-00116118
2002US-0413471P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                          Ishioka G, Fikes J,
                                                                                                                                                                     (EPIM-) EPIMMUNE INC
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                                                                         WO2003087126-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                      Homo sapiens
                                                                                                                                       05-APR-2002;
26-SEP-2002;
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                                            Synthetic
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ADG38664
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                                                                                                                                                                                                                                                                                                 Producing analogs of Major Histocompatibility Complex (MHC) class I peptide epitopes, for treating viral diseases or cancer, comprise producing an analog having (semi)conservative amino acid substitutions of the MHC class I epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a method for producing a polypeptide that contains an analogue of a major histocompatability complex (MHC) class I peptide epitope, wherein the analogue has enhanced immunogenicity compared to the MHC class I peptide epitope. The method of the invention is useful for producing an analogue or heteroclitic analogue of an MHC class I peptide epitope, and eliciting an immune response. The method is useful for preparing MHC class I peptide epitope analogues that can be used to treat viral diseases, cancer and other conditions characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by displayed antigens on target cells. The present amino acid sequence represents a peptide of the invention which is derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mouse; HLA-A24-restricted cancer antigen; antigen; cancer;
tumour suppressor protein; cytostatic; WT1; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 23; DB 7; Length 10; 100.0%; Pred. No. 1.56+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 14; SEQ ID NO 102; 244pp; English.
                                                                                                                                                                     Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO24401 standard; peptide; 10 AA.
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                                                                                                                                                                 Tangri S,
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20-SEP-2002; 2002JP-00275572.
05-APR-2002; 2002US-00116118.
26-SEP-2002; 2002US-0413471P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gotoh M,
                                                                                                                                                                 Ishioka G, Fikes J,
                                                                                                   (EPIM-) EPIMMUNE INC.
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Best Local Similarity
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The present invention relates to antigenic peptides derived from tumour suppressor protein WT1 which induce HLA-A24 restricted cytotoxic T-lymphocytes. The peptides can be used in the preparation of cancer vaccine for treatment and prevention of cancer, including leukaemia, multiple myeloma, lymphoma, and cancer of the stomach, colon, breast, liver, ovary, skin, pancreas, prostate and womb. The present sequence is a polypeptide used in the exemplification of the invention
Antigenic peptides derived from WT1 which induce HLA-A24 restricted cytotoxic T-lymphocytes for production of cancer vaccine and treatment and prevention of cancer.
                                                                                                          Disclosure; Page 97; Opp; Japanese
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Sequence 10 AA;

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Length 10;
                          0; Indels
      Score 23; DB 8; L
Pred. No. 1.5e+02;
23.5%; Sco...
100.0%; Pred. No...
0; Mismatches
                           4; Conservative
      Query Match
Best Local Similarity
                                               NGTF 36
                                                33
                          Matches
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Gaps ö

NGTF 10

MHC class I epitope of human carcinoembryonic antigen, 9-5-4. ADM12345 standard; peptide; 10 AA (first entry) 20-MAY-2004 ADM12345; RESULT

antigen presentation enhancing hybrid polypeptide; mammalian li-Key; MHC class II; antibacterial; virucide; fungicide; antirheumatic; antiarthritic; neuroprotective; dermatological; immunosuppressive; antiinflammatory; antidabetic; antithyroid; immune; rheumatoid arthritis; multiple sclerosis; lupus erythematogus; diabetes mellitus; myasthenia gravis; autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus.

Homo

US2003235594-A1.

25-DEC-2003.

17-SEP-2002; 2002US-00245871

14-SEP-1999; 99US-00396813. 17-JUL-2002; 2002US-00197000. 14-SEP-1999;

(ANTI-) ANTIGEN EXPRESS INC

Xu M; Humphreys R,

WPI; 2004-070554/07.

Novel Ii-Key/antigen presentation enhancing hybrid polypeptide, useful for treating infections, rheumatoid arthritis, multiple sclerosis, lupus erythematosus and diabetes mellitus.

Example 9; Page 34; 87pp; English.

polypeptide. The novel polypeptide has an N-terminal element consisting of 4-16 residues of a mammalian Ii-Key peptide and its non-N-terminal deletion modifications, a chemical structure covalently linking the N-terminal element to an MHC class Is presented epitope of a C-terminal element. The C-terminal element comprises an antigenic epitope, which binds to an antigenic peptide binding site of an MHC class II molecule. The invention relates to a novel antigen presentation enhancing hybrid

The invention relates to a non-naturally occurring protein or polypeptide (I) modified by recombinant DNA techniques comprising: a C-terminal element comprising an MHC Class II-presented epitope; an N-terminal element comprising an II-key motif; and an intervening element comprising a sequence of 4-11 amino acid residues where the modification by recombinant DNA techniques taking place within elements (b) and (c). Also

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The antigen presentation enhancing hybrid polypeptide has the following activities antibacterial, virucide, fungicide, antirhematic, antirhematic, antirhematic, neuroprotective, dermaclogical, immunosuppressive, antiinflammatory, antidiabetic, and antithyroid. The antigen presentation enhancing hybrid polypeptide is useful for modulating the immune response in an individual and for treating infections (such as bacteria, virus, parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus erythematocous, diabetes mellitus, mysathenia gravis, aucoimmune thyroiditis, scleroderma, dermatompositis and pemphigus. This sequence represents a mammalian Ii key related peptide epitope of the invention.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non-naturally occurring protein or polypeptide modified by recombinant DNA techniques, useful for treating multiple sclerosis, diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis, colltis, cancer or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carcinoembryonic antigen (CEA) MHC class II-presented epitope #23
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                                                                                                                                                                                                                                               Length 10;
                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                             23.5%; Score 23; DB 8; Le
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Page 35; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO38565 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-294259/27.
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                              7 NGTF 10
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                                                                                                                                                                                                             Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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directed toward an WHC (major histocompatibility complex) Class II—

C directed toward an WHC (major histocompatibility complex) Class II—

C presented epitope of interest. Suppressing an immune response directed toward an WHC (lass II presented epitope of interest comprises: providing an uncleic acids sequence encoding the WHC Class II—

C amino acids upstream from the N-terminal residue of the MHC Class II—

C manno acids upstream from the N-terminal residue of the MHC Class II—

D presented epitope of interest; and modifying the II.*Key motif. Enhancing an interest comprises: providing a nucleic acid sequence encoding the WHC Class II—

C inmune response directed toward an MHC Class II—presented epitope of interest comprises: providing a nucleic acid sequence encoding the WHC Class II—presented epitope of interest; and modifying to a II.*Key motif located 4-11 amino acids upstream from the N-terminal creation of the MHC Class II—presented epitope of interest; and modifying the nucleic acid sequence to introduce an II-key motif appropriately spaced from the MHC Class II—presented epitope of interest; and modifying the nucleic acid sequence to introduce an II-key motif appropriately spaced from the MHC Class II-presented epitope of interest; and modifying the nucleic acid sequence to introduce an II-key motif appropriately spaced from the MHC Class II-presented epitope of interest; and modifying protein or polypeptide of interest corresponds to a protein or polypeptide encoded by an infectious pathogen selected from anthrax, EBOLA HIV or influenza, polypeptide (I) modified by recombinant DNA techniques is useful for treating infectious diseases caused or associated with infection by a gaptum, virus, parasite, fungus, rickettsia or other infection by a collerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis, allergic rhinitis, topical dermatilis, cancer, psoriasis or adenomas. The present sequence represents the amino acid sequence of invarious interest contractions in the present sequence represe
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described are methods for: suppressing or enhancing an immune response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope; HLA-Al; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44; tumour associated antigen peptide; cytostatic; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.5%; Score 23; DB 8; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HLA-A24 epitope vaccine peptide SeqID265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP80010 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-2003; 2003WO-US038949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-2002; 2002US-0432017P.
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Best Local Similarity 100.vv
Best Local Similarity 100.vv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-468809/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
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                                             This invention relates to a novel isolated peptide which comprises at least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given in the specification. The peptide comprises HIA-A1, A2, A3, A24, B7 or B44 tumour associated antigen peptide. The invention may be useful for the production of compounds with a cytostatic activity or for the production of a vaccine. The peptide is useful in preparing a composition diagnosing or treating tumour associated antigen-related disease. The present sequence is that of an epitope peptide for use in the peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide homologue or analogue with constrained conformation - has proline residues flanking the interaction site to impart greater, or more stable,
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taste modifier peptide; food; drink; sweet; sour; interaction site; constrained conformation; miraculin; curculin.
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                                                                                                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taste modifier peptide (TM-MIR2) contg. proline brackets.
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                             DB 8; Le
1.5e+02;
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                             23.5%; Score 23; 100.0%; Pred. No.
                Claim 1; SEQ ID NO 265; 244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR67090 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 33; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US004294.
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93US-00143364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                         Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evans HJ, Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EVAN/) EVANS H J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KINI/) KINI R M.
                                                                                                                                                                                                                                                                                                                                 33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                                NGTF 10
                                                                                                                                                                                                                              Sequence 10 AA;
                                                                                                                                                                                            the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9425482-A1.
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30-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR67090
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desirable effects on an interaction site. (Also see AAR67011-88 and AAR67092-152 for analogues of other biologically active peptides contg. an interaction site flanked by conformation constraining gps., eg. RGD peptides.) (Updated on 25-MRR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atheroscleroslis; archolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obesty; human immunodeficiency virus infection; HIV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immungen; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human G-protein coupled receptor HGPRBMY11 polypeptide or
polynucleotide, useful for preventing, treating or ameliorating e.g.
myocardial infarction, angina, thrombosis, Alzheimer's disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barber LE;
                                                                                                                                                                         0; Indels
                                                                                                                                     23.5%; Score 23; DB 2; Length 12; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HGPRBMY11 asparagine glycosylation site #1.
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                                                                                                                                                 100.0%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                     ABU11918 standard; peptide; 12 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       schizophrenia, AIDS, leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000US-0249613P.
21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-2001; 2001WO-US044019.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feder J, Nelson TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-093137/08.
                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                  33 NGTF 36
                                                                                                 Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200286123-A2.
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                                                                                                                                                                                                                                                                                                                                                                                            ABU11918;
                                                                                                                                       Query Match
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the method of (8); and (10) screening for candidate compounds capable of binding to and/or medulating activity of a GPCF. The polypeptide or the polympic or and/or medulating activity of a GPCF. The polypeptide or the polympic or and/or medical condition particularly cardiovascular diseases or disorders, or g. myocardial infarction, congestive heart failure, arrhythmisa, cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina, thrombosis or hypertension). The HGPRBW11 polypeptide or polymucleotide is also useful for treating, preventing or ameliorating e.g. Alzheimer's disease, Parkinson's disease, osteoporosis, obesity, human immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness, culflammations, psoriasis, Gaucher's disease or ischaemia (many other diseases and disorders are listed in the specification). The present estimations who most an expession of an HGPRBWX11 protein (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ligands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one CD66 family polypeptide and/or at least one ligand of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of T-
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD66; CEACAM; adhesion molecule; antiviral; antibacterial; antiinflammatory; cytostatic; neutrophil activation; proliferation; differentiation; cancer; angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                  23.5%; Score 23; DB 6; Le 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                            variant) which may be used as an immungen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB88073 standard; peptide; 14 AA
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                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SKUB/) SKUBITZ K M.
(SKUB/) SKUBITZ A P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD66 peptide CD66c-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-234981/24.
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           NGTF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200113937-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skubitz KM,
                                                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB88073;
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
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cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of epithelial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides and adhesion of CD66 family polypeptides to other ligands. The peptides are useful for delivering a therespeutically active agent to a patient, for modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering cell adhesion to a biomaterial, for detecting tumours, for detecting inflammation, for detecting a CD66 protein or its ligand, for altering angiogenesis by contacting endothelial cells, tumour cells or immune cells, for altering an immune response, and for altering keratinocyte proliferation
             88888888888888888
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Sequence 14 AA;

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Gaps
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23.5%; Score 23; DB 4; Length 14; 100.0%; Pred. No. 2.1e+02;
                       0; Indels
      100.0%; Pred. ...
                       4; Conservative
          Local Similarity
Query Match
                       Matches
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33 NGTF 36 NGTF

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AAB88018 standard; peptide; 14 AA.

(first entry) 17-MAY-2001 AAB88018;

CD66 peptide CD66a-18.

CD66; CEACAM, adhesion molecule, antiviral, antibacterial, antiinflammatory, cytostatic, neutrophil activation; proliferation, differentiation, cancer, angiogenesis.

Unidentified

WO200113937-A1 01-MAR-2001. 25-AUG-2000; 2000WO-US023482.

99US-0150791P. 26-AUG-1999; 02-SEP-1999;

SKUBITZ K M. SKUBITZ A P N. (SKUB/) (SKUB/)

Skubitz KM, Skubitz APN;

WPI; 2001-234981/24.

The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ligands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one CD66 family polypeptide and/or at least one ligand of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of Testivation or inhibition, proliferation and/or differentiation of Testivation or inhibition and/or differentiation of Ferentiation of System cells, proliferation and/or differentiation of epithelial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides and adhesion of CD66 family polypeptides co other ligands. The peptides are useful for delivering a therapeutically active agent to a patient, for Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation. Claim 1; Page 39; 102pp; English.

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The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ligands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one compared, were identified that modulate the function of at least one compared are capable of modulating activation of the polypeptide. The peptides are capable of modulating activation of neutrophils, cativation or inhibition, proliferation and/or differentiation of Testing mealls, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of Epithenial cells, homerypic and/or heterotypic adhesion among CD66 family polypeptides to other ligands. The peptides are useful for delivaring a therapeutically active agent to a patient, for modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering angiogenesis by contacting endothelial cells, tumour cells or immune cells, for altering
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modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering cell adhesion to a biomaterial, for detecting inflammation, for detecting a CD66 protein or its ligand, for altering angiogenesis by contacting endothelial cells, tumour cells or immune cells, for altering an immune cells, for altering an immune cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation.
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD66; CEACAM; adhesion molecule; antiviral; antibacterial; antiinflammatory; cytostatic; neutrophil activation; proliferation; differentiation; cancer; anglogenesis.
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Pred. No. 2.1e+02;
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                                                                                                                                                    23.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       AAB88099 standard; peptide; 14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                       4; Conservative
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(SKUB/) SKUBITZ A P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD66 peptide CD66e-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-234981/24.
                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                          33 NGTF 36
                                                                                                                                                                                                                                                                          3 NGTF 6
                                                                                                                               Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                           AAB88099;
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Indels

100.0%; Pred. No. 2.1e+02; 0; Mismatches

4; Conservative

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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 injands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one CD66 family polypeptide and/or at least one ligand of the polypeptide. The peptides are capable of modulating activation of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of T-cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of Equiphalial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides are useful for delivating a therapeutically active agent to a patient, for modifying the metastasis of malianant cells, for altering bacterial or viral binding to cells or malianant cells, for altering abdresion to a biomaterial, for altering andiogenesis by contacting andothelial cells, tumoure sells or immune cells, for altering an immune response, and for altering keratinocyte proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation.
                                                                  Gaps
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an immune response, and for altering keratinocyte proliferation
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                                          Length 14
                                                                 0; Indels
                                         Score 23; DB 4; Le
Pred. No. 2.1e+02;
0; Mismatches 0;
                                 23.5%; sc.
100.0%; Pred
0; M
                                                                                                                                                                       AAB88056 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 43; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                               25-AUG-2000; 2000WO-US023482.
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                                                                                                                                                                                                                   (first entry)
                                Query Match
Best Local Similarity 100...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skubitz APN;
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SKUBITZ A P N.
                                                                                                                                                                                                                                        CD66 peptide CD66b-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-234981/24.
                                                                                       33 NGTF 36
                                                                                                             NGTF 6
                     Sequence 14 AA;
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02-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
                                                                                                                                                                                            AAB88056;
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(SKUB/)
                                                                                                                                               RESULT 36
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23.5%; Score 23; DB 4; Length 14;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide from a surface exposed region of a CD66 family member, useful for modulating the function of CD66 family members, e.g. activation of neutrophils, for treating or diagnosing autoimmune diseases or cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; CD66; CBACAM; cytostatic; antiinflammatory; immunomodulator;
antibacterial; virucide; gene therapy; vaccine; neutrophil;
immune system; autoimmune disease; cancer; infection; bacterial; virus;
inflammatory disease; transplantation; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CD66 family modulating peptide SEQ ID NO 119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 15; 96pp; English.
                                                                                                                                                                                                                                                  ABP67248 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2002; 2002WO-US005720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2001; 2001US-0272113P
                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SKUB/) SKUBITZ K M. (SKUB/) SKUBITZ A P N.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and as a vaccine.
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33 NGTF 36
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                                                                                                                                                                          RESULT 37
ABP67248
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G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arreriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obesity; human immunodeficiency virus infection; HIV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia;
                                                                                                              Human; immungen; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide, useful for preventing, treating or ameliorating e.g. myocardial infarction, angina, thrombosis, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                              human G-protein coupled receptor HGPRBMY11 polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                     Cacace AM, Barber LE;
                                                                                         Human HGPRBMY11v1 asparagine glycosylation site #1.
                                                                                                                                                                                                                                                                                                                                                                                     Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 79; 444pp; English.
                    ABU11935 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     schizophrenia, AIDS, leukemia.
                                                                                                                                                                                                                                                                                                               17-NOV-2000; 2000US-0249613P.
21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                          16-NOV-2001; 2001WO-US044019
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Feder J, Nelson TC,
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093137/08
                                                                                                                                                                                                                                            WO200286123-A2
                                                                                                                                                                                                                      Homo sapiens
                                                                   13-FEB-2003
                                                                                                                                                                                                                                                                   31-OCT-2002,
                                            ABU11935;
RESULT 38
            ABU11935
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The invention relates to an isolated polypeptide (designated HGPRBMY11), which has a G-protein coupled receptor (GPCR) activity (also known as GPCR4 or GPREN1 and is encoded by the cONA contained in ATC Deposit.

Number PTA-2766, its variants (HGPBMY11v1 and HGPRBMY11v2), fragments, domains, species homologues and proteins 95% similar to it. Also included are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including variants, fragments, complements and sequences 95% similar to the HGPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host cells expressing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5) diagnosing a pathological condition in a subject; (6) identifying an activity in a biological assay; (8) a process for making polypucleotide sequences encoding agene product having altered GPCR activity; (9) a shuffled polymucleotide product binding to and/or modulating activity; (7 a GPCR. The polypeptide or the CD binding to and/or modulating activity; (7 a GPCR. The polypeptide or the polymucleotide is useful for preventing, treating or ameliorating a medical condition, particularly cardiovascular diseases or disorders, cardiomyopathy, atherosclerosis, arteriosclerosis, arthribus, cardiomyopathy, atherosclerosis, arteriosclerosis, arteriosclerosis, arteriosclerosis, arteriosclerosis, arteriosclerosis, arteriosclerosis, arteriosclerosis, arteriosclerosis, cardiomyopathy, humans, parkingor, a disease, parkingor, a disease, parkingor, a disease, parkingor, adisease, parkingor, a disease, Parkinson's disease, osteoporosis, obseity, human immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness, acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis, inflammations, psoriasis, Gaucher's disease or ischaemia (many other diseases and disorders are listed in the specification). The present sequence represents a protein motif or domain of an HGPRBMY11 protein (or variant) which may be used as an immungen

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The invention relates to an isolated polypeptide (designated HGPRBMY11), which makes de-protein coupled receptor (GPCR) activity (also known as GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit Number PTA-2766, its variants (HGPRBMY1101 and HGPRBMY1102), fragments, domains, species homologues and proteins 95% similar to it. Also included are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including variants, fragments, complements and sequences 95% similar to the HGPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host Gangnosing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5) diagnosing a pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition in a subject; (6) identifying a binding partner to the HGPRBMY11 polypebtide; (7) identifying an activity in a biological assay; (8) a process for making polynuclectide sequences encoding a gene produced by having altered GPCR activity; (9) a shuffled polynuclectide produced by the method of (8); and (10) screening for candidate compounds capable of binding to and/or modulating activity of a GPCR. The polypeptide or the polynuclectide is useful for preventing, treating or ameliorating a
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obsetty; human immunodeficiency virus infaction; HIV; schlzophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immungen; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       Human HGPRBMY11v1 casein kinase II phosphorylation site #2
                                     Length 14;
                                                                           Indels
                       DB 6; Le...
2.1e+02;
0;
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                         23.5%; bcc.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                            ABU11953 standard; peptide; 14 AA
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21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
                                                                                                                                                                                                                                                                                                                                            (first entry)
                Query Match
Best Local Similarity 100...
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                                                                                                                      33 NGTF 36
                                                                                                                                                         NGTF 9
Sequence 14 AA;
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(1) the nucleic acids encoding the HGPRBMY11 proteins (including

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medical condition, particularly cardiovascular diseases or disorders, e.g. myocardial infarction, congestive heart failure, arrhythmias, cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina, thrombosis or hypertension). The HGPRBMY11 polypeptide or polymucleotide is also useful for treating, preventing or ameliorating e.g. Alzheimer's disease, Parkinson's disease, osteoporosis, obesity, human immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness, acquired immunodeficiency syndrome (AIDS), leukkaemia, sepsis, inflammations, psoriasis, Gaucher's disease or ischemia (many other diseases and discorders are listed in the specification). The present sequence represents a protein motif or domain of an HGPRBMY11 protein (or variant) which may be used as an immungen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polypeptide (designated HGPRBMII), which has a G-protein coupled receptor (GPCR) activity (also known as GPCR74 or GPCRR) and is encoded by the cDNA contained in ATCC Deposit Number PTA-2766, its variants (HGPRBMYIIV1 and HGPRBMYIIV2), fragments, domains, species homologues and proteins 95% similar to it. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obsesty; human immunodeficiency virus infection; HIV; schlzophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; gaucher's disease; lachaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
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                                                                                                                                                                                                                                                                                                23.5%; Score 23; DB 6; Length 14; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HGPRBMY11 N-myristoylation site #1.
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21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     NGTF 14
                                                                                                                                                                                                                                                           Sequence 14 AA;
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The straints, fragments, complements and sequences 95% similar to the GPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host cells expressing HQPRBMY11; (4) an anti-HQPRBMY11 antibody; (5) diagnosing a pathological condition or a susceptibility to a pathological condition in a subject; (6) identifying a binding partner to the Condition in a subject; (6) identifying an activity in a biological assay; (8) a process for making polymucleotide sequences encoding a gene product having altered GPCR activity; (9) a shuffled polymucleotide produced by the method of (8); and (10) screening for candidate compounds capable of binding to and/or modularing activity of a GPCR. The polympeptide or the condition particularly cardiovascular diseases or disorders, condition particularly cardiovascular diseases or disorders, condition particularly cardiovascular diseases or disorders, cardiomyopathy, atherosolerosis, arteriosclerosis, embolism, angina, thrombosis or hypertension). The HGPRBMY11 polypeptide or polymucleotide cardiomyopathy, atherosolerosis, osteoporosis, obesity, human immunodeficiency virus (HIV) infections, schizophrenia, sepsis, cardiomactions, psoriasis, Gaucher's disease or ischeamia, sepsis, inflammations, psoriasis, Gaucher's disease or ischeamia, sepsis, inflammations, psoriasis, disease or ischeamia, sepsis, inflammations, psoriasis, disease or ischeamia, sepsis, inflammations, psoriasis, disease or ischeamia (many other capariant) which may be used as an immungen
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100..
... 4; Conservative
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Search completed: February 24, 2005, 15:19:36 Job time : 130.463 secs

4 NGTF 7

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US-09-902-540-13360

| Sequence 13360, Application US/09902540
| Patent No. 6833447
| GENERAL INFORMATION:
| APPLICANT: Goldman, Barry S.
| APPLICANT: Goldman, Barry S.
| APPLICANT: Hinkle, Gregory J.
| APPLICANT: Wiegand, Roger C.
| TITLE OF INVENTION: Wiegand, Roger C.
| TITLE OF INVENTION: Wiegand, Roger C.
| PILE REPRENCE: 38-10(15849)B
| CURRENT PILING DATE: 2001-07-10
| PRIOR APPLICATION NUMBER: US/09/902,540
| CURRENT PILING DATE: 2000-07-10
| PRIOR PILING DATE: 2000-07-10
| PRIOR PILING DATE: 2000-07-10
| SEQ ID NO 13360
| LENGTH: 103
US-09-902-540-10583
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Best Local S:
Matches 7
TYPE: PRT
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Sequence 13360, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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9, Appli
60291, A
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                                                                                                          February 24, 2005, 15:14:52; Search time 28.2276 Seconds (without alignments) 148.094 Million cell updates/sec
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3. /cgn2_6/ptodatca/1/iaa/6B_COMB.pep:*

3. /cgn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-902-540-13360

US-08-194-290-7

US-08-614-377A-7

US-08-873-479-44

US-08-973-479-44

US-08-973-422-83

US-08-933-402-83

US-08-933-402-83

US-08-931-797-83

US-08-931-797-83

US-08-931-797-83

US-08-931-492-83

US-08-931-492-83

US-08-931-997-928-90

US-08-931-997-928-90

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US-09-270-767-60291

US-09-97-792A-19

US-09-97-792A-19

US-09-915-965A-1420

US-09-915-965A-1420

US-09-9515-965A-1420

US-09-350-641C-1420
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 1419,
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Sequence 1419,
Sequence 1242,
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US-09-315-304B-1419
US-09-350-641C-1419
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US-09-082-279B-1242
US-09-315-965A-1984
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US-09-350-641C-1747
US-09-350-641C-1748
US-09-350-641C-1748
US-09-350-841A-1936
US-09-350-841A-1937
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ALIGNMENTS

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Sequence 10583, Application US/09902540

Fatent No. 683347

GENERAL INPORMATION:

APPLICANT: Gladman, Barry S.

APPLICANT: Gladman, Barry S.

APPLICANT: APPLICANT: Steven C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849) B.

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 60/217,883

PRIOR PLING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 10583
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0; Mismatches 17; Indels
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Similarity 29.2%;
7; Conservative (
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GENERAL INFORMATION:
APPLICANT: Smit, John
APPLICANT: Smit, John
APPLICANT: Smit, John F.
APPLICANT: Bingle, Wadde H.
APPLICANT: No. 6210946ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULOF
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULOF
CURRENT APPLICATION NUMBER: US/09/142,648B
CURRENT FILING DATE: 1999-03-30
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1996-03-12
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                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,377A
FILING DATE: 12-MAR-1996
CLASSIFICATION 435
PRIOR APPLICATION THE:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/895,367
FILING DATE: 09-UNB-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FEBO. Y. ROCKY
REGISTRATION NUMBER: 34053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1026
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                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 NGTFXXXXXXXXXXXXGDXXXXG 56
                         Richardson PC
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                                         225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1026 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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US-09-142-648B-7
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                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08194290
Patent No. 5500353
GENERAL INFORMATION:
APPLICANT: Smit, John
APPLICANT: Hingle, Wade H
TITLE OF INVENTION: Bacterial surface protein expression
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: 3000 South Eads Street
                                                                  DB 4; Length 103;
                                                                25.5%; Score 25; DB 4; Length 103
29.2%; Pred. No. 1.5e+02;
tive 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08614377A
Fatent No. 597664
GENERAL INFORMATION:
APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: PETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTER
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Felease #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garvey, George A
REGISTRATION NUMBER: 17737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6e+03;
                                                                                                                                                                                                                                                                                                                                                                                          LU Burface protei
LU Shlesinger, Arkwright & Garvey
STREET: 1000 South Eads Street
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB
Pred. No. 1.6e
0; Mismatches
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                                                                                                                                                                                                69 NGTFVNGEKVKQSRLKEGDRILIG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 NGTFXXXXXXXXXXGDXXXXG
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-836-5288
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
; ORGANISM: Myxococcus xanthus US-09-902-540-13360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1026 amino acids
                                           Query Match
Best Local Similarity 29.27
Best Local 7; Conservative
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Best Local Similarity 25.0
Matches 6; Conservative
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// MOLECULE TYPE: protein
US-08-194-290-7
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US-08-614-377A-7
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Sequence 83, Application US/08933402
| Patent No. 5948887
| GENERAL INFORMATION:
| APPLICANT: EVANS, Herbert J. APPLICANT: KINI, R. Manjunatha | TITLE OF INVENTION: Polypeptides That Include Conformation-TITLE OF INVENTION: Site | NUMBER OF SEQUENCES: 153 | CORRESPONDENCE ADDRESSE: Foley & Lardner | ADDRESSEE: Foley & Lardner | STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                          COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08.532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-ACT-1993
PRIOR APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOGTWARE: Patentin Release #1.0, Version #1.25
SUGRESSY APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-5EPT-1997
PRIOR APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.5%; Score 23; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                        : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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Matches 4; Conservative
                                                             ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
    Washington
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-934-222-83
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US-08-933-402-83
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Sequence 83, Application US/08934222
Sequence 83, Application US/08934222
Sequence 83, Application US/08934222
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardner
STREET: Suite 500, 3000 K Street NW
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                           Gaps
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                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide TITLE OF SOUTHORS: 57
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: No. 58917010 ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 2; Length 418;
Pred. No. 1.1e+03;
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                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFICATION: 530
ATTORNAY AGENT INFORMATION:
NAME: AGTIS, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/POCKET NUMBER: 5.51.000-US
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
Similarity 25.0%; Pred. No. 1.6e+03; 6; Conservative 0; Mismatches 18
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                                                                                                      267 NDTFVAGEVAGAATLTVGDTLSGG 290
                                                             33 NGTFXXXXXXXXXXXG 56
                                                                                                                                                                                                               Sequence 44, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 NGTYRVADFSSRGHKTAGD 325
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.5%;
26.3%;
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LENGTH: 418 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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Matches 5; Conservative
  Best Local Similarity
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Sequence 83, Application US/09231797

Patent No. 6084066

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction S.
NUMBER OF SEQUENCES.
ADDRESSEE: Foley & Lardner
                                                                                                                                                                  Sequence 83, Application US/08532818
Sequence 83, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
STREET: D.
STATE: D.
STATE: D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/051,741
FILING DATE: 23-APR-1993
ATTOMEY/AGENT: NUMBER: US. 08/051,741
FILING DATE: 23-APR-1993
ATTOMEY/AGENT: NUMBER: US. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.5%; Score 23; DB 2;
100.0%; Pred. No. 45;
tive 0; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 33,751
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 12 amino acids
amino acid
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Isacson, John P
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 NGTF 36
                           33 NGTF 36
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                                                                                                                                                         US-08-532-818-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 83, Application US/09207621
Patent No. 5552465
GENERAL INFORMATION:
APPLICANT: ETANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                23.5%; Score 23; DB 2; Length 12;
                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: USA

CIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/207,621

FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294

FILING DATE: 13-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US. 08/143,364

FILING DATE: 20-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US. 08/143,364

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAMME: ISAGEON, JOHN P.

REGISTRATION NUMBER: 33.751

REFERENCE/DOCKET NUMBER: 33.751

REFERENCE/DOCKET NUMBER: 33.751

REFERENCE/DOCKET NUMBER: 33.751
                                                                                                                                                                                                                                                                                                                             100.0%; Preu. ...
                                                                                      NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERNCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILLING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, JOHN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 amino acids
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-207-621-83
                                                                                                                                                                                                                                                                  US-08-933-402-83
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US-08-933-843-83

US-08-933-843-83

Sequence 83, Application US/08933843

Sequence 83, Application US/08933843

Sequence 84, Application US/08933843

Sequence 85, Application US/08933843

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: EVANS, Herbert J.

APPLICANT: EVANS, Manjunatha

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

TITLE OF INVENTION: Site

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STREET: DC
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/33,843
FILING DATE: 19-SEPT-1997
FILING DATE: 19-SEPT-1997
FILING DATE: 03-MAY-1996
FILING DATE: 20-CT-1993
FILING DATE: 20-CT-1993
FILING DATE: 23-APR-1993
FILING DATE: 23-APR-1993
FILING DATE: 23-APR-1993
FRIOR APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTER/SICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. Active 10, Mismatches
                   FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         040433/0148
PCT/US94/04294
                                                                                                                                                                                                      NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              23.5%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                        ropology: linear
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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Sequence 83, Application US/08934224
Sequence 83, Application US/08934224
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, K. Marjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
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Pred. No. 45;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
FILING DATE: 21-APR-1994
FILING DATE: 22-CT-1993
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTOMNEY/AGENT INFORMATION:
NAME: 18ac80n, John P.
REFERENCE/DOCKET NUMBER: 33,751
REGISTRATION NUMBER: 33,751
REGISTRATION NUMBER: 33,751
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INPORMATION FOR SEQ ID NO: 83:
SEMEMBER: 12-APRACTERISTICS:
SEMEMBER: 12-APRACTERISTICS:
SEMEMBER: 12-APRACTERISTICS:
Suite 500, 3000 K Street NW
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
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Best Local Similarity
Matches 4; Conserva
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GY: linear
                        Washington
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                                                                   USA
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                                                                                       20007
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Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interaction
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APPLICANT: Blain, Francoise
APPLICANT: Blain, Francoise
APPLICANT: Bennett, Clark
APPLICANT: Zimmermann, Joseph
APPLICANT: Zimmermann, Joseph
APPLICANT: AND Su, Kangfu
APPLICANT: Zimmermann, Joseph
APPLICANT: Mucleic Acid Sequences And Expression
TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
TITLE OF INVENTION: Flavobacterium heparinum
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
CORRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/413,492
FILING DATE: 08/512,818
FILING DATE: 08/512,818
FILING DATE: 21-APR-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1996
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
FILING DATE: 23-APR-1993
ATTONNENYAGERT INFORMATION:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTONNENYAGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
TITLE OF INVENTION: Polypeptides That .
TITLE OF INVENTION: Constraining Groups TITLE OF INVENTION: Site NUMBER OF SEQUENCES: 153 CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner STREET: Suite 500, 3000 K Street NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08258639A Patent No. 5681733 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 83: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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US-08-934-223-83
is Sequence 83, Application US/08934223
j Faquence 81, Application US/08934223
j Fatent No. 6147189
j GENERAL INFORMATION:
j APPLICANT: EVANS, Herbert J.
j APPLICANT: EVANS, Herbert J.
j TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
j TITLE OF INVENTION: Site
j TITLE OF INVENTION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                    DB 3; Length 12;
45;
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                                                                                                                               0; Indels
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ZIP: 20007
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 3;
Pred. No. 45;
                                             23.5%; Scor.
100.0%; Pred. No. -..
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PRIOR APPLICATION NUMBER: US/08/532,818
PRIOR APPLICATION DATA:
PREDICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REPERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-413-492-83
; Sequence 83, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
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                                                              Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: IBEX TECHNOLOGIES and
APPLICANT: ISEX TECHNOLOGIES and
APPLICANT: INFORMANN, Joseph
TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
TITLE OF INVENTION: Plavobacterium heparinum
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
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Patent No. 6703491
GENERAL INFORMATION
THORMATION SET APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 23
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CURRENT APPLICATION DATA:
APPLICATION VMBER: PCT/US95/07391A
FILING DATE: 09-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
. 89;
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89;
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STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20004.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 23.5%; Score 23; DB
100.0%; Pred. No. 89;
ative 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,639
FILING DATE: 10 JUNE 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                Query Match
Best Local Similarity 100.v
Para 4; Conservative
                                                   23 amino acids
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Best Local Similarity 100...
4; Conservative
                               SEQUENCE CHARACTERISTICS
                                                                                                         ; MOLECULE TYPE: peptide US-08-900-951-9
                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                  33 NGTF 36
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US-09-270-767-60291
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PCT-US95-07391A-9
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APPLICANT: Su, Hongsheng
APPLICANT: Blain, Francoise
APPLICANT: Bennett, Clark
APPLICANT: Gu, Kangfu
APPLICANT: Zimmermann, Joseph
APPLICANT: Zimmermann, Joseph
TITLE OF INVENTION: Nucleic Acid Sequences And Expression
TITLE OF INVENTION: Plavobacterium heparinum
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and Dorr
STREET: 1455 parrer:
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Pred. No. 89;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U50.8945
CLASSIFICATION 1944
CLASSIFICATION WINEER: 36,160
REFERENCY POCKET NUMBER: 36,160
REFERENCY DOCKET NUMBER: 36,160
REFERENCY (202)942-8404
FELECOMMUNICATION INFORMATION:
TELEFONE: (202)942-8404
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TWANE: Amino acids
TWANE: Amino acids
TWANE: Amino acids
TWANE: Amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
PILING DATE: US/08/900,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.5%; Scc. 100.0%; Pred. No. c. 0; Mismatches
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STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Healey, William J.
REGISTRATION NUMBER: 36,160
REFERENCE/DOCKET NUMBER: 104385.116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 942 8400
TELEPAX: (202) 942 8404
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,639
FILING DATE: 10 JUNE 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYRDPERTIES
TITLE OF INVENTION: HYRDPERTIES
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT TAILING DATE: 1999-05-20
FRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1420
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; Sequence 1420, Application US/09082279B
; Patent No. 625879E
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: PHARNACOKINETIC PROPERTIES
; TITLE OF INVENTION: PHARNACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICANTON: WUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1420
; LENGTH: 38
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                                                                                           Query Match 23.5%; Score 23; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                             ; OTHER INFORMATION: Synthetic Construct US-09-997-792A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-315-304B-1420
; Sequence 1420, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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        ; FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/09209799D

Patent No. 6380357

GENERAL INFORMATION

APPLICANT: Horefuling, Ronald

APPLICANT: Hoffmann, James

APPLICANT: Narasinhan, Chakravarthy

ITLE OF INVENTION UNBER: US/09/209,799D

CURRENT FILIAG DATE: 1998-12-11

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.0

LENGTH: 31

LENGTH: 31
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US-09-997-792A-19

Sequence 19, Application US/09997792A

Patent No. 655521

GENERAL INFORMATION:

APPLICANT: ELI LILLY and COMPANY

ITLE OF INVENTION: Glucagon-Like Peptide-1 Crystals

FILE REPERENCE: X-10242A

CURRENT APPLICATION NUMBER: US/09/997,792A

CURRENT APPLICATION NUMBER: US 60/069,728

PRIOR APPLICATION NUMBER: US 60/069,728

PRIOR APPLICATION NUMBER: US 60/069,728

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.1

LENGTH: 31
HATORNEY/AGENT INFORMATION:

NAME: BAKER, Hollie L.

REGISTRATION NUMBER: 31,321

REPERENCE/DOCKET NUMBER: 104385.116PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 942-8484

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENOTH: 23 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: peptide

PCT-US95-07391A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic construct
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Best Local Similarity 100.0
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Best Local Similarity 100.
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ORGANISM: Artificial
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Patent No. 6750008
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: PETHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: PGSION ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7972-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT PILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: Patentin Ver. 2.1
ERQTH: 38
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYRDED POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-067
TITLE OF INVENTION UNMER: 09/9350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: PastsEQ for Windows Version 3.0
SEQ ID NO 1420.
LENGTH: 38
                                                                                         Gaps
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                                          Length 38;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                            Score 23; DB 4; L
Pred. No. 1.5e+02;
                                                                                         0; Mismatches
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Patent No. 6656906
GENERAL INFORMATION:
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                                            23.5%;
100.0%;
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ORGANISM: Artificial Sequence
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                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
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US-09-350-841A-1420
US-09-515-965A-1420
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Patent No. 6623741

GENERAL INFORMATION:
APPLICANT: Balmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Lambert, D.
APPLICANT: Bariekson, J.
APPLICANT: Sista, P.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION:
TITLE OF INVENTION: METHODS AND COMPOSITION SOVERNESSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: 09/315,304
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1420
LENTH: 38
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              23.5%; Score 23; DB 3; Length 38; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                           Sequence 1420, Application US/09834784

Patent No. 6562787;
GENERAL INPORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Dennie
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION NUMBER: US/09/834,784
CURRENT APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE PRESENCE
SOFTWARE: PRESENCE
SOFTWARE: PRESENCE
SOFTWARE: PRESENCE
SOFTWARE: PRESENCE
SOFTWARE: PRESENCE
SEQ ID NOS: 1515
SEQ ID NO 1420
SEQ ID NO 1420
SEG ID NO 1420
SEG ID NO 1420
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
                Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                         33 NGTF 36
                                                                                                                                                      NGTF 15
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US-09-515-965A-1420
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US-09-834-784-1420
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US-09-515-965A-1419
Sequence 1419, Application US/09515965A
PERCENT NO. 6623741
September 10. 6623741
September 10. 6623741
APPLICANT: Antczak, J.
APPLICANT: Belmedico, M.
APPLICANT: Exickson, J.
APPLICANT: Site, Site, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: METHODS AND COMPOSITIONS RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
SEQ ID NO 1419
SEQ ID NO 1419
LENGTH: 39
FUNDRER DATE: 1999-05-20
SEQ ID NO 1419
FUNDRER DATE: 1999-05-20
FUNDRER DATE: 1999-05-20
SEQ ID NO 1419
FUNDRER DATE: 1999-05-20
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                                                                                                                Sequence 1419, Application US/09834784
; Batent No. 6562787
; GENERAL INFRAMITION:
APPLICANT: Barney, Shawn
; APPLICANT: Barney, Shawn
; APPLICANT: Barney, Gene
; APPLICANT: Merutx, Mehmed
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
; TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
; TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
; CURRENT PELLOATION NUMBER: US/09/834,784
; CURRENT APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SEQ ID NO 1419
; LEUTH: 39
; LEUTH: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Core polypeptide US-09-834-784-1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.C
Matches 4; Conservative
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14 NGTF 17
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US-09-315-304B-1419
is Sequence 1419, Application US/09315304B
j Patent No. 6348568
j Fatent No. 6348568
j GENERAL INFORMATION:
j APPLICANT: Barney, S.
j APPLICANT: Anwer, M.
j APPLICANT: Anwer, M.
j APPLICANT: Lambert, D.
j TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
j TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
j TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
j TITLE OF INVENTION: HYBRID POLYPEPTIDES
j CURRENT APPLICATION NUMBER: US/09/315,304B
j CURRENT PILING DATE: 1998-05-20
j RIDR FILING DATE: 1998-05-20
j NUMBER OF SEQ ID NOS: 1667
j SOFTWARE: FastSEQ for Windows Version 3.0
j SEQ ID NO 1419
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                                                                                                                                                                                                                                                Sequence 119, Application US/09082279B
Sequence 119, Application US/09082279B
Sequence No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthite, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
FILE REFERENCE: 7872-043
CURRENT APPLICANTON NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1419
LENGTH: 39
LENGTH: 39
LENGTH: 39
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US-09-082-279B-1419
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
The 4; Conservative
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                               33 NGTF 36
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US-09-082-279B-1419
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APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRER 1980-95-20
CURRENT APPLICATION NUMBER: 09/082,279
FRICR APPLICATION NUMBER: 09/082,279
PRICR APPLICATION NUMBER: 09/082,279
PRICR APPLICATION NUMBER: 09/082,279
PRICR APPLICATION NUMBER: 09/082,279
PRICR APPLICATION NUMBER: 09/082,279
SEQ ID NOS: 1667
SEQ ID NO 1242
LEMCTH. 40
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                                                                         APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7972-043
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 1242
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23.5%; Score 23; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 1.68+02;
Matches 4; Conservative 0; Mismatches 0;
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                   Sequence 1242, Application US/09082279B
Partent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1242, Application US/09834784; Patent No. 6562787
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, OTHER INFORMATION: Core polypeptide
US-09-315-304B-1242
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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  US-09-082-279B-1242
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US-09-834-784-1242
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Patent No. 675008
GENERAL INFORMATION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILLE REFERENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT PILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SEQ ID NO 1419
SEQ ID NO 1419
LEGISTH: 39
                                                                                                                                                                                                                        APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR PLILOR DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FRAELSE FASTES FASTES FOR Windows Version 3.0
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
                                                                                                                                   ; Sequence 1419, Application US/09350641C; Patent No. 6656906; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-841A-1419
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
                                                                                                                                                                                                       APPLICANT: Barney, S. APPLICANT: Guthrie, K. APPLICANT: Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 NGTF 36
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14 NGTF 17
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US-09-350-841A-1419
                                                                                                                  -09-350-641C-1419
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LENGTH: 39
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RESULT 34

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Sequence 1985, Application US/09515965A

Sequence 1985, Application US/09515965A

GENERAL INFORMATION:

APPLICANT: APLICANT: Delmedicc, M.

APPLICANT: Endert, D.

APPLICANT: Endert, D.

APPLICANT: Sieta, P.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE SOURENT PILLING DATE: 1992-05-20

PRIOR PILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1994

SOFTWARE PRESENCE FOR WINDOWS Version 3.0

SEQ ID NO 1985

LENGTH. 40
                             APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Existen, J.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILER REPERENCE: 782-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT PILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PRILING DATE: 1998-05-20
SRIOR FILING DATE: 1998-05-20
SRQ ID NO 1984
SSQ ID NO 1984
LENGTH: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.5%; Score 23; DB 4; Length 40; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: 4, 8
OTHER INFORMATION: Xaa = Abu (aminobutyric acid)
US-09-515-965A-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Core polypeptide US-09-515-965A-1984
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.5°
Best Local Similarity 100.
Matches 4, Conservative
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APPLICANT: Antocak, J.
APPLICANT: Delmedico, M.
APPLICANT: Eleickon, J.
APPLICANT: Eleickon, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: MOMBER: US/09/515,965A
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SEQ ID NO 1242
LENGTH: 40
LENGTH: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.5%; Score 23; DB 4; Length 40; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                     APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
FRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastEEQ for Windows Version 3.0
SEQ ID NO 1242
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US-09-515-965A-1984
; Sequence 1984, Application US/09515965A
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; Sequence 1242, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
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US-09-834-784-1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
Barney, Shawn
Guthrie, Kelly
Merutka, Gene
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14 NGTF 17

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RESULT 40

US-09-350-641C-1242

Sequence 1242, Application US/09350641C

Patent No. 6656906

GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Anwer, M.
APPLICANT: Apple. 199-07-09

PRIOR PLING DATE: 1999-05-20

PRIOR PLING DATE: 1999-05-30

PRIOR PLING DATE: 1999-05-30

TWHER OF SEQ ID NOS: 1757

SOFTWARE: FASTERE,

LENGTH: 40

TYPE: PRT

ORGANISM: Artificial Sequence

TYPE: PRT

OTHER INFORMATION: Core polypeptide

US-09-350-641C-1242
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Best Local Similarity 100.
Matches 4; Conservative
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Search completed: February 24, 2005, 15:25:30 Job time : 30.2276 secs

14 NGTF 17

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Pebruary 24, 2005, 15:23:51 ; Search time 81.0406 Seconds
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226.127 Million cell updates/sec
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1: \( \text{cgn2} \) \( \text{Fprodata} / 2 \) \( \text{pubpa} / \) \( \text{USOVB} \) \( \text{Pubpa} \) \( \text{Pubpa} / \) \( \text{USOVB} \) \( \text{Pubpa} / \) \( \text{Pubpa} / \) \( \text{USOVB} \) \( \text{Pubpa} / \) \( \text{Pubpa} / \) \( \text{USOVB} \) \( \text{Pubpa} / \) \( \text{Pubpa
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1380268 seqs, 327241040 residues
                                                                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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S	Score	Query	* Query Match Length DB	DB	91	Description
1	1					
	25	25.5		16	US-10-652-870-248	Sequence 248, App
	25	25.5		16	US-10-652-870-252	Sequence 252, App
	25	25.5		16	US-10-652-870-250	Sequence 250, App
	25	25.5		6	US-09-379-931-7	Sequence 7, Appli
	25	25.5	1026	14	US-10-223-597-7	Sequence 7, Appli
	52	25.5		17	US-10-478-676-1	Sequence 1, Appli
	23	23.5	6	16	US-10-657-022-194	
	23	23.5	10	15	US-10-245-871-305	305,
	23	23.5	10	15	US-10-296-317-48	48,
	23	23.5		15	US-10-253-286-305	305,
	23	23.5	12	10	US-09-991-225-23	23,
	23	23.5		15	US-10-369-405-23	23,
	23	23.5	14	10	US-09-991-225-42	Sequence 42, Appl

	60,	204	9	Sequence 72, Appl Sequence 606, App	909	909	312	312	67,		1524	Sequence 168021,	2	Sequence 5, Appli	9	급	-	_	_	_	_	Sequence 9, Appli	Sequence 7, Appli	443	Sequence 1243, Ap	Н	Sequence 238104,
0 US-09 5 US-10 5 US-10	60-SN US-09	4 US-10	US-10		5 US-10	US-10	5 US-10-245-6	5 US-10-253-2	US-1	15 US-10-296-317-59	US-10-424-599-152	US-10-424-599-1	US-09-209-799D-22	0 US-09-736-960-5	LO US-09-997-792-22	-995-494	US-10-351-641-14	US-10-351-641-14	-351-641-12	US-10-351-641-17	3-10-35	9 US-09-912-628-9	4 US-10-11	15 US-10-425-114-44378	4 US-10-351-641-1	6 US-10-437-963-1	L5 US-10-424-599-238104
	15 1		15	15		•	• •	•	26 1	28	30	30	31	31	31	37	38 1	39 1	40	40	40						43 1
233.	23 23.5 23 23.5	23.	23.	23.	23.	~	23.	23.	23.	23.	23.	23.	23.	7	23.	23.	23.	23.	3 23.	3 . 23.	3 23.	3 23.	3 23.	23.	3 23.	3 23.	23 23.5
14 15 16	17	19	50	21	23	24	25	56	27	. 58	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 248, Application US/10652870

Sequence 248, Application US/10652870

Sequence 248, Application No. UG20040167068A1

GENERAL INFORMATION:
APPLICANT: Internet Leah
APPLICANT: John, Farley
APPLICANT: Applicant: Applicant: APPLICANT: Bernfield, Liesel
APPLICANT: APPLICANT: Bernfield, Liesel
APPLICANT: Metcalf, Benjamin
TITLE OF INVENTION: Meningococcal Disease
TITLE OF INVENTION: Meningococcal Disease
CURRENT APPLICATION NUMBER: US/10/652,870
FILE REFERENCE: 38523.000026
CURRENT APPLICATION NUMBER: US/10/652,870
FRIOR FILING DATE: 2003-09-02
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin version 3.1
SEQ ID NO 248
LENGTH: 260
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; ORGANISM: Neisseria meningitidis
US-10-652-870-248
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RESULT 2

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APPLICANT: Smit, John
APPLICANT: Smit, John
APPLICANT: Smit, John
APPLICANT: Bigle, Wade H.
APPLICANT: Bigle, Wade H.
APPLICANT: No. US20020009792Alellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULO:
FILE REFERENCE: 08106/002003
CURRENT APPLICATION NUMBER: US/09/379,931
CURRENT FILING DATE: 1996-03-12
PRIOR APPLICATION NUMBER: US 08/194,290
PRIOR FILING DATE: 1994-02-09
PRIOR FILING DATE: 1994-02-09
PRIOR APPLICATION NUMBER: US 07/895,367
PRIOR FILING DATE: 1992-06-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1026
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APPLICANT: Bingle, Wade H.
APPLICANT: Bingle, Wade H.
APPLICANT: Bingle, Wade H.
APPLICANT: No. US2003135037A1ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULOB, FILE REFERENCE: 08106/00203
CURRENT PELLING DATE: 202-08-19
CURRENT PILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: US/09/379, 931
PRIOR PILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR PILING DATE: 1996-03-12
PRIOR PLING DATE: 1996-03-12
PRIOR PLING DATE: 1996-03-12
PRIOR PLING DATE: 1996-06-09
PRIOR PLING DATE: 1992-06-09
PRIOR PELNEN NUMBER: US 07/895, 367
PRIOR PLING DATE: 1992-06-09
SPRIOR PLING DATE: 1992-06-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.5%; Score 25; DB 9; 1
Best Local Similarity 25.0%; Pred. No. 4.5e+03;
Matches 6; Conservative 0; Mismatches 18.
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Publication No. US20030135037A1
GENERAL INFORMATION:
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; Sequence 1, Application US/10478676
; Publication No. US20050032194A1
; GENERAL INFORMATION:
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US-10-223-597-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Caulobacter crescentus US-09-379-931-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-223-597-7
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| Publication No. US20040167068A1
| General Involvation of US20040167068A1
| General Involvation:
| APPLICANT: Clounick, Gary
| APPLICANT: Fletcher, Leah
| APPLICANT: John, Farley
| APPLICANT: John, Farley
| APPLICANT: Metchalf, Menial
| APPLICANT: Metchalf, Menial
| APPLICANT: Metchalf, Menial
| APPLICANT: Metchalf, Menial
| TITLE OF INVENTION: Menial
| TITLE OF INVENTION: Menial
| TITLE OF INVENTION: UNMER: US/10/652,870
| FILE REFERENCE: 38523.00026
| CURRENT APPLICATION NUMBER: US/10/652,870
| PRIOR FILING DATE: 2003-09-02
| PRIOR FILING DATE: 2003-09-02
| PRIOR FILING DATE: 2003-09-02
| WINDBER OF SEQ ID NOS: 329
| SOUTHARE PATCHILIN VERSION 3.1
                                                                                                                 APPLICANT: Zlotnick, Gary
APPLICANT: Zlotnick, Gary
APPLICANT: Zlotnick, Cary
APPLICANT: Zlotnick, Leah
APPLICANT: Bernield, Liesel
APPLICANT: Bernield, Liesel
APPLICANT: Zagursky, Robert
APPLICANT: Zagursky, Robert
APPLICANT: Zagursky, Robert
APPLICANT: Mercalf, Benjamin
TITLE OF INVENTION: Movel Immunogenic Compositions for the Prevention and Treatment of INVENTION: Movel Immunogenic Compositions for the Prevention and Treatment of INVENTION: Movel Immunogenic Compositions for the Prevention and Treatment of INVENTION WOMBER: US/10/652,870
PRIOR APPLICATION NUMBER: US 10/652,870
PRIOR APPLICATION NUMBER: US 10/652,870
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin version 3.1
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Best Local Similarity 25.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 18; Indels
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                        ; Sequence 252, Application US/10652870; Publication No. US20040167068A1; GENERAL INFORMATION:
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; Patent No. US20020009792A1
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ORGANISM: Neisseria meningitidis
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ORGANISM: Neisseria meningitidis
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US-10-652-870-250
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US-10-652-870-252
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LENGTH: 260
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LENGTH: 261
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US-09-379-931-7
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33 NGTF 36
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Sequence 305. Application US/10245871
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT PILING DATE: 2003-01-09
PRIOR PILING DATE: 2002-07-17
                                   APPLICANT: BINGLE, Wade, H.

TITLE OF INVENTION: PROTEASE DEFICIENT CAULOBACTER HOST CELLS
FILE REFERENCE: 3225-199048
CURRENT APPLICATION NUMBER: 2003-11-24
PRIOR PILING DATE: 2003-11-24
PRIOR PILING DATE: 2002-22
PRIOR PILING DATE: 2001-05-22
PRIOR PILING DATE: 2001-05-22
PRIOR PILING DATE: 2001-05-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1026
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FUDDICATION NO. US20040180354A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Zhengor
FILE REFERENCE: MANNK.032A
CURRENT APPLICATION WUMBER: US/10/657,022
CURRENT FILING DATE: 2003-09-04
PRIOR APPLICATION NUMBER: 60/409123
PRIOR APPLICATION NUMBER: 60/409123
PRIOR APPLICATION NUMBER: 60/409123
PRIOR SEQ ID NOS: 610
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 NDTFVAGEVAGAATLTVGDTLSGG 290
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                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Caulobacter crescentus US-10-478-676-1
                       NOMELLINI, John, F.
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; ORGANISM: Homosapiens
US-10-657-022-194
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Best Local Similarity
Matches 6; Conserva
APPLICANT: SMIT, John
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US-10-245-871-305
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Publication No. US2004005881A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: HUMPHREYS, ROBERT

TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REPREBENCE: EBH-2015

CURRENT APPLICATION NUMBER: 10/197,000

PRIOR PILING DATE: 2003-01-13

PRIOR PLING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: PATENTIN OF: 2.1

SEQ ID NO 305

LENGTH: 10
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is Sequence 48, Application US/10296317

j Publication No. US20040057968A1

j GENERAL INFORMATION:

j APPLICANT: CEI-Sci Corp

j APPLICANT: Satin, Prem S

TILLE OF INVENTION: T CELL BINDING LIGAND PEPTIDE

j PILE REFERENCE: CS-112

CURRENT FILING DATE: 2002-11-22

CURRENT FILING DATE: 2000-05-24

j PRIOR PELING DATE: 2001-05-24

j PRIOR APPLICATION NUMBER: PCT/US07/16793

j PRIOR PILING DATE: 2001-05-24

j NUMBER OF SEQ ID NOS: 96

s SOFTWARE: Patentin version 3.1

j EDATE: 10 48
                                                                                                                                                                                                                      Query Match 23.5%; Score 23; DB 15; Length 10; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 305
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US-10-296-317-48
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-305
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NSCOULTS. 42

1 Sequence 42, Application US/0991225

2 Sequence 42, Application US/0991225

3 Sequence 42, Application US/0991225

3 Sequence 42, Application US/0991225

4 Publication NO. US20030153063A1

5 GENERAL INFORMATION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI

7 TITLE OF INVENTION: HEART AND VARIANTS THEREOF

7 TITLE OF INVENTION: HOWBER US/09/991,225

7 CURRENT APPLICATION NUMBER: 60/249,613

PRIOR PLING DATE: 2000-11-16

9 PRIOR APPLICATION NUMBER: 60/257,611

PRIOR PILING DATE: 2000-12-21

9 PRIOR FILING DATE: 2000-12-21

9 PRIOR FILING DATE: 2001-10-6

9 PRIOR FILING DATE: 2001-07-16

10 NUMBER OF SEQ ID NOS: 81

10 SEQ ID NO S: 81

11 ENGTH: 14
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US-09-991-225-69

Sequence 69, Application US/09991225

Sequence 69, Application US/09991225

Publication No. US20030153063A1

GENERAL INFORMATION:

APPLICANT: Bristol-Wyers Squibb Company

ITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBWY11, EXPRESSED HI

TITLE OF INVENTION: HEART AND VARIANTS THEREOF

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBWY11, EXPRESSED HI

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBWY11, EXPRESSED HI

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN G-P
                                                                        Gaps
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      Length 12;
                                                                    Indels
Query Match 23.5%; Score 23; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-991-225-42
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US-09-991-225-69
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US-10-369-405-23

US-10-369-405-23

Sequence 23, Application US/10369405

Publication No. US2003224400A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY11, AND VARIANTS

TITLE OF INVENTION: THEREOF

FILE REFERRANCE: D0075A CIP

CURRENT APPLICATION NUMBER: US. 60/249,613

PRIOR APPLICATION NUMBER: U.S. 60/249,613

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2000-10-21

PRIOR PELING DATE: 2000-10-21

PRIOR PELING DATE: 2000-10-21

PRIOR PELING DATE: 2000-10-21

PRIOR PELING DATE: 2001-07-16

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PatentIn version 3.2

SEQ ID NO 23

LENGTH: 12
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TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
FILE REPERBNCE: D0075. NP
CURRENT APPLICATION NUMBER: US/09/991,225
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
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                                                                                                    23.5%; Score 23; DB 15; Length 10; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
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Pred. No. 1.7e+02;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                    Query Match
Best Local Similarity 100.0
These 4; Conservative
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Matches 4; Conservative
   ; ORGANISM: Homo sapiens
US-10-253-286-305
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US-09-991-225-23
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; ORGANISM: homo sapiens
US-10-369-405-23
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US-09-991-225-23
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Sequence 60, Application US/09991225

Sequence 60, Application US/09991225

Sequence 60, Application US/09991225

Publication No. US20030153063A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myears Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTBIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HIGHTLE OF INVENTION: A NOVEL HUMAN G-PROTBIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HIGHTLE OF INVENTION: A NOVEL HUMAN G-PROTBIN COUPLED REPRENCE: 2001-11-16

FILE REFERENCE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/249,613

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-11-21

SPRIOR FILING DATE: 2000-11-31

SPRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin version 3.0

LENGTH. 15
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; Sequence 72, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICATY: Britatol-Myers Squibb Company
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; TITLE OF INVENTION: HOPER TON UNDER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; FRIOR PAPLICATION NUMBER: 60/249,613
; PRIOR PAPLICATION NUMBER: 60/257,611
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR APPLICATION NUMBER: 60/305,818
; RIOR APPLICATION NUMBER: 60/305,818
; PRIOR APPLICATION NUMBER: 2001-07-16
; PRIOR APPLICATION NUMBER: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/305,818
; SOFTWARE PATENTING DATE: 2001-07-16
; SEQ ID NO 72
: LENGTH: 15
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Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.5%; Scott 100.0%; Pred. No. 2...
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ilarity 100.0%;
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Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Homo sapiens
US-09-991-225-60
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Best Local Similarity
Matches 4; Conserv
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11 NGTF 14
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                                                                                                                                                                                                           ## Sequence 42, Application US/10369405
## Sequence 42, Application US/10369405
## Sequence 42, Application No. US20030224400A1
## GENERAL INFORMATION
## APPLICANT: Bristol-Myers Squibb Company
## TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, AND VARIANTS
## TITLE OF INVENTION: THEREOF
## CURRENT APPLICATION NUMBER: US/10/369,405
## CURRENT APPLICATION NUMBER: US. 60/249,613
## PRIOR PLING DATE: 2000-11-17
## PRIOR PLING DATE: 2000-11-17
## PRIOR PLING DATE: 2000-12-21
## PRIOR APPLICATION NUMBER: U.S. 60/257,611
## PRIOR PLING DATE: 2000-12-21
## PRIOR APPLICATION NUMBER: U.S. 60/305,818
## PRIOR PLING DATE: 2000-10-16
## NUMBER OF SEQ ID NOS: 94
## SOFTWARE: PATENTING DATE: 2001-07-16
## NUMBER OF SEQ ID NOS: 94
## SOFTWARE: PATENTING DATE: 2001-07-16
## SOFTWARE: PATENTING DATE: 2001-07-16
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| Genemic 69, Application US/10369405
| Publication No. US20030224400A1
| GENERAL INFORMATION:
| APPLICANT Bristol-Hydres Squibb Company | TITLE OF INVENTION: THEREOF | TITLE OF INVENTION WINDER: U.S. 60/249,613 |
| PRIOR PILING DATE: 2000-11-17 | PRIOR PPLICATION NUMBER: U.S. 60/257,611 |
| PRIOR PILING DATE: 2000-12-21 | PRIOR PPLICATION NUMBER: U.S. 60/257,611 |
| PRIOR PILING DATE: 2000-12-21 |
| PRIOR FILING DATE: 2000-10-16 |
| NUMBER OF SEQ ID NOS: 94 |
| SOFTMARE: PATENTIN VERSION 3.2
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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NGTF 14
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   NGTF 36
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US-10-369-405-69
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RESULT 19

33 NGTF 36

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TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, AND VARIANTS;
TITLE OF INVENTION: THEREOF;
FILE REFERENCE: D0075A CIP;
CURRENT APPLICATION NUMBER: US/10/369,405;
CURRENT FILING DATE: 2003-02-14;
PRIOR APPLICATION NUMBER: U.S. 60/249,613;
PRIOR APPLICATION NUMBER: U.S. 60/249,613;
PRIOR APPLICATION NUMBER: U.S. 60/249,613;
PRIOR PILING DATE: 2001-11-16;
PRIOR APPLICATION NUMBER: U.S. 60/257,611;
PRIOR PILING DATE: 2001-22;
PRIOR PILING DATE: 2001-22;
PRIOR PILING DATE: 2001-01-6;
PRIOR APPLICATION NUMBER: U.S. 60/305,818;
PRIOR PILING DATE: 2001-07-16;
NUMBER OF SEQ ID NOS: 94;
SOFTWARE: PatentIn version 3.2;
LENGTH: 15
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US-09-962-756-606

Sequence 606, Application US/09962756

Publication No. US20030195147A1

GENERAL INFORMATION:
APPLICANT: PILLUTLA, RENUKA
APPLICANT: BRISSETTE, RENEE
APPLICANT: BRISSETTE, RENEE
APPLICANT: GOLDSTEN, NEIL I.
APPLICANT: SCHAFFER, JANG
APPLICANT: SPETZLER, JANG
APPLICANT: SPETZLER, JANG
APPLICANT: NOWERN: USCUS
APPLICANT: SPETZLER, JANG
APPLICANT: SPETZLER, JANG
APPLICANT: SCHAFFER, JANG
APPLICANT: SPETZLER, JANG
APPLICANT: OSTERGAARD, SOREN
APPLICANT: SPETZLER, JANG
APPLICANT
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US-09-962-756-606
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Matches 4; Conserv
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                                     gequence 2046, Application US/10225567A

publication No. US2033113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: LifeSpan Biosciences
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Rough, Christine L.
TILE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR PLICALION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTHARE: Patentin version 3.1
SEQ ID NO 2046
LENGTH: 15
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publication No. US20030224400A1

GENERAL INDORMATION:
TITLE OF INVENTION: WOUEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY11, AND VARIANTS
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 2.1e+02;
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Sequence 72, Application US/10369405
Publication No. US20030224400A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%; 5c.
100.0%; Pre
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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US-10-369-405-60
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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21 NGTF 24
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Fublication No. US20040023887A1

GENERAL INFORMATION:

APPLICANT: PILLUTLA, RENUKA et al.

FILE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS

FILE REPERENCE: 1878 4056

CURRENT APPLICATION NUMBER: US/10/253,493

CURRENT FILING DATE: 2002-09-24

PRIOR APPLICATION NUMBER: 09/523,756

PRIOR PILING DATE: 2001-09-24

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1998-09-02

NUMBER OF SEQ ID NOS: 2227

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 606

LENGTH: 18
              Sequence 606, Application US/10253471

Publication No. US20030236190A1

GENERAL INFORMATION:

APPLICANT: PILLUTIA, RENUKA et al.

TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS

TITLE OF INVENTION INVENTION AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS

CURRENT PILLING DATE: 2002-09-24

PRIOR PILLING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 09/962,756

PRIOR APPLICATION NUMBER: 09/962,756

PRIOR APPLICATION NUMBER: 09/146,127

PRIOR PILLING DATE: 2000-03-29

PRIOR FILING DATE: 1998-09-02

NUMBER OF SEQ ID NOS: 2227

SOFTWARE: PATCHIN VOY: 2.1
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US-10-253-471-606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-253-493-606
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 4; Conservative
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Matches 4; Conserva
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US-10-253-471-606
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RESULT 25 US-10-245-871-312

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Sequence 312, Application US/10253286
; Sequence 312, Application US/10253286
; Publication No. US2004005881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR FILING DATE: 1003-01-13
; PRIOR FILING DATE: 199-09-14
; NUMBER OF SEQ ID NOS: 905
; SEQ ID NO 312
; LENGTH: 24
Sequence 312, Application US/10245871

Publication No. US20030235594A1

GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: HUMPHREYS, ROBERT
TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: ERH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2003-01-09
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 1999-09-14
FRIOR FILING DATE: 1999-09-14
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FEATURE:
NAME/KEY: MOD_RES
IOCATION: (5)
OTHER INFORMATION: a-aminovaleric acid
FEATURE:
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FEATURE:
NAME/KEY: MOD_RES
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US-10-245-871-312
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Sequence 168021, Application US/10424599
| Sequence 168021, Application US/10424599 |
| Publication No. US/0040031072A1 |
| Publication No. US/0040031072A1 |
| APPLICANT: La Rosa Thomas J |
| APPLICANT: La Royalic David K |
| APPLICANT: Zhou Yihua |
| APPLICANT: Cao Yongwai |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: David K |
| TITLE OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Zhow Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 152465
LENGTH: 30
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US-10-424-599-152465
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US-10-424-599-168021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 23; DB 15; I 100.0%; Pred. No. 4.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                           US-10-424-599-152465
; Sequence 152465, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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US-09-209-799D-22
; Sequence 22, Application US/09209799D
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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                                               33 NGTF 36
                                                                                                      25 NGTF 28
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US-10-424-599-168021
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Publication No. US20040057968A1
GENERAL INFORMATION:
APPLICANT: CELSCI Corp
APPLICANT: Zimmerman, Daniel S
APPLICANT: Zimmerman, Daniel S
APPLICANT: Zimmerman, Daniel S
APPLICANT: Sain, Prem S
ITILE OF INVENTION: T CELL BINDING LIGAND PEPTIDES, FILE REFERENCE: CS-112
CURRENT APPLICANTON NUMBER: US/10/296,317
CURRENT FILING DATE: 2002-11-22
FRIOR APPLICATION NUMBER: US 60/206548
FRIOR APPLICATION NUMBER: PCT/US07/16793
FRIOR FILING DATE: 2001-05-24
FRIOR APPLICATION NUMBER: PCT/US07/16793
FRIOR FILING DATE: 2001-05-24
FRIOR APPLICATION NUMBER: PCT/US07/16793
FRIOR FILING DATE: 2001-05-24
INWHER OF SEQ ID NOS: 96
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59, Application US/10296317
Publication No. US20040057968A1
| GENERAL INFORMATION:
| APPLICANT: CLIP Corp |
| APPLICANT: Zimmerman, Daniel S |
| APPLICANT: Zimmerman, Daniel S |
| APPLICANT: Zimmerman, Daniel S |
| APPLICANT: Simmerman, Daniel S |
| APPLICANT: Simmerman, Daniel S |
| APPLICANT: Simmerman, Daniel S |
| APPLICANT: Zimmerman, Daniel S |
| TITLE OF INVENTION: T CELL BINDING LIGAND PEPTIDES |
| FILE REFERENCE: CS-112 |
| CURRENT APPLICATION NUMBER: US/10/296,317 |
| CURRENT FILING DATE: 2000-05-24 |
| PRIOR APPLICATION NUMBER: PCT/US07/16793 |
| PRIOR APPLICATION NUMBER: PCT/US07/16793 |
| NUMBER OF SEQ ID NOS: 96 |
| SEQ ID NO 59 |
| LENGTH: 28 |
| LENGTH: 28 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.5%; Score 23; DB 15; Length 26; 100.0%; Pred. No. 3.6e+02; Live 0; Mismatches 0; Indels
             Length 24;
                                                                           0; Indels
      23.5%; Score 23; DB 15; I 100.0%; Pred. No. 3.3e+02; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                           Conservative
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Matches 4; Conserv
Query Match
Best Local Similarity
Matches 4; Conserv
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NGTF 26
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US-10-296-317-59
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APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
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Best Local Similarity 100.
Matches 4; Conservative
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Sun, Yongming
Liu, Chenghua
Chen, Sei-Yu
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; ORGANISM: Homo sapien
US-09-995-494-113
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Best Local Similarity
Matches 4; Conserv
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US-09-995-494-113
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APPLICANT:
APPLICANT:
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APPLICANT: Garman, Jonathan David
APPLICANT: Garman, Jonathan David
APPLICANT: Candia III, Albert Frederick
APPLICANT: Candia III, Albert Frederick
APPLICANT: Arbor vite Corporation
TITLE OF INVENTION: CLASP-5 Transmembrane Protein
FILE REFERENCE: 020054-000511US
CURRENT APPLICATION NUMBER: US 60/160,860
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR FILING DATE: 1999-10-29
PRIOR PALLING DATE: 1999-10-29
PRIOR PALLING DATE: 1999-10-29
PRIOR PALLING DATE: 1999-10-29
PRIOR PALLING DATE: 2000-01-14
PRIOR PALLING DATE: 2000-01-14
PRIOR PALLICATION NUMBER: US 60/196,267
PRIOR PALLING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR PALLING DATE: 2000-04-11
PRIOR PALLING DATE: 2000-04-11
PRIOR PALLING DATE: 2000-04-11
PRIOR PALLING DATE: 2000-04-11
PRIOR PALLICATION NUMBER: US 60/196,528
PRIOR PALLICATION NUMBER: US 60/196,528
PRIOR PALLING DATE: 2000-10-13
                                            APPLICANT: Hermeling, Ronald
APPLICANT: Hoffmann, James
APPLICANT: Hoffmann, Chakravarthy
TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
FILE REFERENCE: X-10242
                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/209,799D CURRENT FILING DATE: 1998-12-11 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin version 3.0 SEQ ID NO 22 LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: SYNThetic construct US-09-209-799D-22
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APPLICATION NUMBER: US 60/240,543
FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09736960
Patent No. US20020102267A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter
Publication No. US20010014666A1
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Chen, Sei-Yu
TTLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0.293
CURRENT APPLICATION NUMBER: US/09/995,494
FURRENT FILING DATE: 2000-111-27
PRIOR APPLICATION NUMBER: 60/253,176
PRIOR PILING DATE: 2000-115
SOFTWARE: PatentIn version 3.1
SSQ ID NOS: 115
SSQ ID NO 113
LENGTH: 37
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                                                                                                                                                                            Length 31;
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Publication No. US20030045464A1

GENERAL INFORMATION:
APPLICANT: Hermeling, Ronald
APPLICANT: Narasimhan, Chakravarthy
TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
FILE REPERBUCE: X-10242
CURRENT APPLICATION NUMBER: US/09/997,792
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
                                                                                                                                                                         23.5%; Score 23; DB 9; Le
100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0;
; SEQ ID NO 5
; LENGTH: 31
; TYPE: PRT
; OTGANISM: Homo sapiens
; OTHER INFORMATION: preliminary human CLASP-5
US-09-736-960-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: SYNTHETIC CONSTRUCT US-09-997-792-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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33 NGTF 36
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SEQ ID NO 1419
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WESULT 35

Sequence 1420, Application US/10351641

Publication No. US20303086874A1

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Anwer, M.

APPLICANT: Anwer, M.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

CURRENT APPLICATION NUMBER: US/10/351,641

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 1757

SEQ ID NO 1420

SEQ ID NO 1420
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APPLICANT: Barney, S.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRE: US/10/351,641
CURRENT FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR SEQ ID NOS: 1757
SOPTWARE: FastSEQ for Windows Version 3.0
                                                               Gaps
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                   Length 37;
                                                             0; Indels
               Score 23; DB 9;
Pred. No. 5e+02;
    23.5%; Scor.
100.0%; Pred. No. scor.
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Core polypeptide US-10-351-641-1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                 Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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12 NGTF 15
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APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutek, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
PRIOR PAPLICATION NUMBER: 09/350,641
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
SPRIOR FILING DATE: 1998-05-20
SPRIOR FILING DATE: 1998-05-30
SOFTWARE: FastSEQ for Windows Version 3.0
SSQ ID NO 1242
LENGTH: 40
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, S.
APPLICANT: Lambert, M.
APP
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100.0%; Pred. No. 5.3e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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; Publication No. US20030186874A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1242, Application US/10351641 Publication No. US20030186874A1 GENERAL INFORMATION:
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                                                                                                                                                     CTHER INFORMATION: Core polypeptide US-10-351-641-1419
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.(
Matches 4; Conservative
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APPLICANT: Guthrie, K.
APPLICANT: Anwer, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Lamber, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRE: US/10/351,641
TITLE OF INVENTION NUMBER: US/10/351,641
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PLILING DATE: 1999-05-20
PRIOR PLILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
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Pred. No. 5.4e+02;
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; OTHER INFORMATION: Xaa = Abu (aminobutyric acid)
US-10-351-641-1748
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100.0%; Pred. No. .
0; Mismatches
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1748, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Core polypeptide US-10-351-641-1747
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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NAME/KEY: SITE
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; Sequence 9, Application US/09912628 ; Patent No. US20020160491A1 ; GENERAL INFORMATION:

RESULT 40 US-09-912-628-9

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TLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (32)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , LOCATION: (33)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-912-628-9
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100.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 0;
              TILE REPRENCE: PT001P2
CURRENT APPLICATION NUMBER: US/09/912,628
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/02484
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US00/05082
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-3
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 24, 2005, 15:42:01 Job time : 83.0406 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 NGTF 36
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

February 24, 2005, 15:12:40; Search time 21.8537 Seconds (without alignments) 246.555 Million cell updates/sec

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description			probable secreted	130K paracrystalli	paracrystalline su	S-layer protein Rs	prepilin [imported	transferrin-bindin	hypothetical prote	Rhs element associ	_	63	TINIE	alpha-1-acid glyco	>	colicin V precurso	Ig upsilon chain -	hypothetical prote	hypothetical cytos	opacity protein op	probable membrane	hypothetical prote	ď	yijD protein - Esc		hypothetical prote	B. subtilis YhdG p	B. subtilis YhdG p	gntR-fam	hypothetical prote	
SUMMARIES	ΩI	:	D70986	T34986	-11	A48995	C87374	AG1028	D81832	E81911	E85731	D96953	T40973	A96525	B26300	A82829	B82829	S43147	E69223	AD3596	S44709	AD0935	D86088	G91240	G65203	S21565	E97103	AD1123	AF1483	T36750	D64339	
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	.* Query Match Length		865	220	312	1026	1073	435	698	42	49	57	83	84	102	102	102	110	111	112	116	119	119	119	. 119	120	121	123	132	134	135	
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138 138	141 143 143	143 143 144	146 147 151	152 156	156 157 158
23.5	23.5 23.5 23.5	23.5 23.5 23.5	23.5 23.5 53.5	23.5	23.5 23.5
23	2333	2333	5333	23	2333
30 31	33 33 4	35 37	8 8 4 8 6 0	41 42	4 4 4 4 4 5 5 4 3

ALIGNMENTS

RESULT 1 D70986 probable ABC transporter Rv1747 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: D70986 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; ; Connor, R.; Davies, R.; Devlhin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H; Rajandream, M.A.; Rogers, J.; Ruteer, S.; Seeger, K.; Skelton, S.; Squares, S.

; Gordon, S Holroyd, S.

Nature 393, 537-544, 1998
Alauthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70986
A;Accession: D70986
A;Residues: DNA
A;Residues: 1-865 <COL>
A;Cross=references: UNIPROT:065934; GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CAB09333.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rx1747
C;Superfamily: Mycobacterium tuberculosis probable ABC transporter Rv1747; ATP-binding C
C;Keywords: ATP
F;335-528/Domain: ATP-binding cassette homology <ABC>

. 0 Query Match 28.6%; Score 28; DB 1; Length 865; Best Local Similarity 29.2%; Pred. No. 70; Matches 7; Conservative 0; Mismatches 17; Indels 33 NGTFXXXXXXXXXXXGDXXXXG 56 ò

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Gaps

270 NGTFVNGARVDAALLHDGDVVTIG 293

probable secreted protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Bate: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34986
R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
S;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Reference number: Z21550
A;Accession: T34986
A;Accession: T34986
A;Accession: T34986
A;Accession: T34986
A;Accession: T320 coll>
A;Cross-references: UNIPROT:O86667; EMBL:AL031182; PIDN:CAA20163.1; GSPDB:GNO0070; SCOED
C;Genetics:

RESULT 2

g

A; Gene: SCOEDB: SC4A2.11c

us-09-936-956-1.rpr

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Query Match
Best Local Similarity 25.0%;
Matches 6; Conservative (
                                                                                                                                                                25.5%;
ilarity 25.0%;
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Similarity 25.0%;
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Best Local Similarity
The 6; Conserva
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-698 <PAR>
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      A; Accession: C87374
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A48995

paracrystalline surface layer protein RsaA - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Gilchrist, A.; Fisher, J.A.; Smit, J.
Can. J. Microbiol. 38, 193-202, 1992
A;Title: Nucleotide sequence analysis of the gene encoding the Caulobacter crescentus pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1026 <GIL>
A; Residues: 1-1026 <GIL>
A; Cross-references: UNIPROT: P35828; GB:AF062345; GB:M22663; GB:M84760; NID:g6064104; PID
A; Experimental source: CB15A, ATCC 19089
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:116173, NCBIP:116174)
                                                                                                                                                                                                                   130K paracrystalline protein - Caulobacter crescentus (fragment)
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: O'Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Mar-1998
C;Accession: A31846
R;Fisher, J.A.; Smit, J.; Agabian, N.
J. Bacteriol. 170, 4706-4713, 1988
A;Title: Transcriptional analysis of the major surface array gene of Caulobacter crescentations A;Reference number: A31846; MUID:89008089; PMID:3049545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 2; Length 312;
Pred. No. 1.5e+02;
0; Mismatches 18; Indels
25.5%; Score 25; DB 2; Length 220; 26.3%; Pred. No. 18+02; tive 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-312 <FIS>
A;Cross-references: GB:M22663; NID:g556033; PID:g556034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 NDTFVAGEVAGAATLTVGDTLSGG 288
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                                                                                                                      158 HGTFTTLEGSTVTTSGSGD 176
                                                                                33 NGTFXXXXXXXXXGD 51
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                                        Conservative
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A;Status: preliminary
A;Molecule type: nucleic acid
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Best Local Similarity
Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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Cjaccesion: AG1028

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

AjAuthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove, A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Mature 404, 502-506, 200.
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:068937; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85244
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transferrin-binding protein B NMA2025 [imported] - Neisseria meningitidis (strain Z2491 C;bpcdes Neisseria meningitidis C;bates Neisseria meningitidis C;bate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C;Accession: 081832
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C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepilin [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1073 <STO>
A;Residues: 1-1073 <STO>
C;Genetics:
C;Genetics:
A;Gene: CC1007
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A;Cross-references: GB:AL513382; PIDN:CAD09328.1; PID:g16505328; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 5.8e+02;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 2; Length 435
Pred. No. 3.6e+02;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                    Score 25; DB 2; 1
Pred. No. 4.9e+02;
0; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                          33 NGTFXXXXXXXXXXXG 56
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A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A,Reference number: A96900, MUID:21359325, PMID:21359325
                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 «KUR»
A;Cross-treferences: UNIPROT:Q97LW9; GB:AE001437; PIDN:AAK78415.1; PID:g15023290; GSPDB:G
A;Experimental source: Clostridium acetobutyllcum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA.
XResidues 1.83 -LIXN>
A;Cross-references: UNIRROT:094581; EMBL:AL031966; PIDN:CAA21442.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h-; cosmid c1442
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Liu, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luxos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome c oxidase polypeptide vib - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                Length 57;
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C;Superfamily: mammalian cytochrome-c oxidase chain VIb
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                23.5%; Score 23; DB 2;
100.0%; Pred. No. 89;
:ive 0; Mismatches
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                   Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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                                                               A; Accession: D96953
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                                                                                                                                                                                 B81911

hypothetical protein NWA1420 [imported] - Neisseria meningitidis (strain Z2491 serogroup C;Species Neisseria meningitidis
C;Species Neisseria meningitidis
C;Accession: B81911

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Nature 404, S02-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9JUA3; GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB8466
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession ES5731
C;Accession ES5731
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Mature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157;H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E85731
Rhs element associated protein Z2255 [imported] - Bscherichia coli (strain O157:H7, subs
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A;Experimental source: strain 0157:H7, substrain EDL933
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: D96953
R;Nolling, J:; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
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                                      33 NGTFXXXXXXXXXXGDXXXXG
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-49 <STO>
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A,Gene: Z2255
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Silveira
A.L.; Za
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82829
C;Accession: B282829
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9PGN5; GB:AE003879; GB:AE003849; NID:g9105067; PIDN:AAF83070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rismpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; All Briones, M.S.; Bueno, M.R. Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.S.; Bueno, M.R. Camargo, A.A.; Fanaro, L.E.A.; Carraro, D.M.; Carrer, H submitted to Genbank, June 2000
A.A. Athors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohmel A.A. Madeira, M.L.; Kemper, E.L.; Kitcijma, J.P.; Karieger, J.E.; Kuramae, E.E.; Laigre, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.A.; Oliveira, M.R.; Matsukuma, A.Y.; Menck, C.F.N.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Aluthors: da Silva, A.C.R.; da Silva, A.C.R.; da Silva, A.N.; Silva Jr., W.A.; da Silva, F.R.; Vallada, S.J., Vettore, A.L.; Za, A.R. Feference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig upsilon chain - duck (fragment)
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Accession: S43147
R;Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
R;Magor, K.E.; Higgins, Library, March 1994
A;Reference number: S446ance from duck immunoglobulin genes that IgY is the common ancestor of A;Reference number: S43145
A,Recossion: S43147
A;Status: preliminary
A;Molecule type: DNA
           Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Alatuhors: da Silva, A.C.R.; da Silva, A.G.R.; Silva Jr., W.A.; da M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A;Reference number: A59328
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                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                            A;Contents: annotation C;Genetics: A;Gene: XF0262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
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A88829
collicin V precursor XF0262 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Accession: A88229
Collicin A88229
C;Accession: A88229
A;Accession: A88225; Multiple Consortium of the Organization for Nucleotide Sequentary A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A88229
A;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-102 <CCO>
A;Cross-references: UNIPROT:091X23
A;Experimental source: strain SWR/J
C;Comment: At least 2 genes coding for different forms of alpha-1-AGP appear to be prese
C;Comment: Alpha-1-AGP is synthesized in the liver, the synthesis being controlled by gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-1-acid glycoprotein (clone pMAGP3) - mouse (fragment)
NyAlternate names: orosomucoid
C;Speciaes: Mus musculus (house mouse)
C;Speciaes: Mus musculus (house mouse)
C;Accession: B26300
R;Cooper, R.; Papaconstantinou, J.
S;Cooper, R.; Papaconstantinou, J.
S;Cooper, R.; Papaconstantinou, J.
A;Title: Evidence for the existence of multiple alpha-1-acid glycoprotein genes in the A;Reference number: A26300; MUID:86111861; PMID:3003086
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C;Keywords: acute phase; glycoprotein; liver; plasma
F;1-101/Domain: lipocalin homology (fragment) <LIP>
F;8-101/Disnifide bonds: #status predicted
F;8-101/Disnifide bonds: #status predicted
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                                                                                                                  23.5%; Score 23; DB 2; Length 84; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
                                                                               Query Match
Best Local Similarity 100.
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A; Map position: 1
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opacity protein opaB - Neisseria meningitidis (isolate 21213) (fragment)
C;Species: Neisseria meningitidis
A;Variety; isolate 21213
C;Date: 13-Jan-1995 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: 844709
Mol. Microbiol. 12, 171-180, 1994
A;Title: Microbiol. 12, 171-180, 1994
A;Title: Microevolution within a clonal population of pathogenic bacteria: recombination
A;Reference number: $44705; MUID:94335637; PMID:7520117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:051089; EMBL:U03409; NID:g432174; PIDN:AAA61550.1; PID:g4321 A;Experimental source: isolate Z1213; strain serogroup A; clone pFLOB2510 A;Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein
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R;Parkhil, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servo, A;Reference number: AB0502; MUID:21534947; PMID:11677608
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hypothetical protein yijD [imported] - Escherichia coli (strain O157:H7, substrain EDL93
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A;Cross-references: GB:AL513382; PIDN:CAD09502.1; PID:g16504619; GSPDB:GN00176
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1.8e+02;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypotheeical protein MTH922 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Bate: O5-Dec-1997 #sequence Tevision O5-Dec-1997 #text_change 09-Jul-2004
C;Accession: E6923
R;Smith, D.R; poucette-Stamm, L.A.; Deluughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
K;Smith, D.; Spadafora, R.; Vicaire, R.; Wano, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
K; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: E6923
A;Accession: E6923
A;Accession: E6923
A;Accession: E6923
A;Accession: E69223
A;Accession:
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A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AD3596
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:1175688
A;Accession: AD3596
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical cytosolic protein BMEI10693 [imported] - Brucella melitensis (strain 16M)
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                                      A;Cross-references: EMBL:X78355; NID:g468612; PID:g468613
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                         23.5%; Score 23; DB 2; Length 110; 100.0%; Pred. No. 1.7e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 2; Length 111;
Pred. No. 1.7e+02;
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                         Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
A;Residues: 1-110 <MAG>
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A;Map position: II
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A;Start codon: TTG
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C; Species: Clostridium acetobutylicum
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C; Accession: E97103
C; Accession: E97103
R; Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A; Reference number: A96900; MUID:21359325; PMID:21359325
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A;Experimental source: Clostridium acetobutylicum ATCC824
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CjDate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
CjAccession: AD1123
RjGlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P27308; EMBL:X66026; NID:943236; PIDN:CAA46824.1; PID:943239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein B - Bscherichia coli
C;Species: Escherichia coli
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S1565
R;Gustafsson, C.
submitted to the EMBL Data Library, May 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein CAC1650 [imported] - Clostridium acetobutylicum
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                                                                                             Length 119;
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                     DB 2; Le
. 1.8e+02;
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                                                                                         Query Match 23.5%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 4; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 4; Conservative
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A;Accession: S21565
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A, Status: preliminary
                                                                                                                                                                                                                                                           33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary A;Molecule type: DNA
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            A, Gene: yijD
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G65203

yijb protein - Bscherichia coli (strain K-12)

C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Becies: Bscherichia coli
C;Becies: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Bate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: G65203
R;Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 4433-4657, 1997
A;Title The complete genome sequence of Bscherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G65203
A;Accession: G65203
A;Accession: G65203
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-119 < BNA
A;Residues: 1-110 < BNA
A;Residues: 1-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22

dg91240

hypothetical protein ECs4895 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G91240
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Tele: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: poreliminary
A;Mesiduse: 1-119 etAty.
A;Residuse: 1-110 etAty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P27308; GB:AE005174; NID:g12518891; PIDN:AAG59168.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Feb-2001
R;Parna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Tritle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A88480; MUID:21074935; PMID:11206551
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Pred. No. 1.8e+02;
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100.0%; Pred. No. ...
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4, Conserva
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A,Molecule type: DNA
A,Residues: 1-119 <STO>
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A,Gene: yijD
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Query Match 23.5
Best Local Similarity 100.
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Best Local Similarity
1, Conserve
       A; Gene: SCOEDB: SCI11.17c
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Science 294, 849-852, 2001

A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A,Authors: Schlueter, T.; Sinoes, N.; Tisterraz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listerraz species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD113
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-133 cGLA>
A;Kesidues: 1-133 cGLA>
A;Cross-references: UNIPROT:Q8Y9Y0; GB:NC_003210; PIDN:CAC98466.1; PID:g16409765; GSPDB:A;Experimental source: strain EGD-e
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C;Dates: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Datesion: A;Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: ABIO77; MUID:21537279; PMID:11679669
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A;Cross-references: UNIPROT:Q92EQ3; GB:AL592022; PIDN:CAC95638.1; PID:g16412834; GSPDB:G
A;Experimental source: strain Clip11262
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36750
R;Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21613
A;Accession: T36750
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Gene: 1mo0387
C;Superfamily: Bacillus subtilis hypothetical protein ydhG
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Best Local Similarity 100.
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AF1483
B. subtili
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Cjaccession: D64339
RjBult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.Bult, C.J.; White, O.; Ousbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Facich, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Auchors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
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A; Molecule type: DNA
A; Residues: 1-138 «KUUR»
A; Cross-references: UNIPROF: Q97WZ9; GB: AEO06641; NID: g13815234; PIDN: AAK42152.1; GSPDB: G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyporhetical protein MJ0315 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                 Gaps
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llarity 100.0%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 0;
DB 2; L
2.1e+02;
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C;Superfamily: conserved hypothetical protein MJ0315
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                                                                                                                 0; Mismatches
     Score 23;
Pred. No.
23.5%;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <HAY>
A; Gene: NCSP: B23L21.20
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A.Gene: PH1621
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A;Cross-references: UNIPROT:Q08687; EMBL:Z75160; NID:g1420570; PID:e252106; PID:g1420571
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 33
T49689
T49689
Whyothetical protein B23L21.20 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49689
R;Accession: T49689
R;Accession: T49689
R;Accession: T49689
R;Accession: T49689
A;Reference number: Z2502
C;Genetics: DAA
A;Residues: DAA
A;Residues: DAA
A;Residues: 1-143 <CCH>
C;Genetics:
                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q22499; EMBL:Z68880; PIDN:CAA93096.1; GSPDB:GN00022; CESP:T1
A;Experimental source: clone T14G10
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                hypothetical protein T14G10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24916
R;Wild, A.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19954
A;Reference number: Z19954
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-138 <WIL>
A;Residues: 1-138 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S67149

hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae)

hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae)

NyAlternate names: hypothetical protein 05310

C;Species: Saccharomyces cerevisiae

C;Bate: 12-7u1-1996 #sequence_revision 12-Ju1-1996 #text_change 09-Ju1-2004

C;Accession: S67149

R;Jauniaux, J.C.; Poirey, R.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Cross-references: SGD:S0005778
A;Map position: 15R
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 NGTF 118
                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:T14G10.4
A;Map position: 4
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hypothetical protein ECB3799 [imported] - Escherichia coli (strain O157:H7, substrain RIN
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: G91103

C; Accession: G91103

C; Adyashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

DNA Res. 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A; Reference number: A99629; MUID:21156211; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q8XDO2; GB:BA000007; PIDN:BAB37222.1; PID:g13363271; GSPDB:GN
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
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A;Molecule type: DNA
A;Residues: 1-143 <KAW>
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A;Map position: 6
A;Introns: 67/3; 80/2
C;Superfamily: Neurospora crassa hypothetical protein B23L21.20
                                                                                                                                                Query Match 23.5%; Score 23; DB 2; Length 143; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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hypothetical protein ybbK - Bacillus subtilis
                                    A; Cross-references: UNIPROT: Q7M222
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Best Local Similarity
Lag 4; Conserve
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A; Molecule type: mRNA
A; Residues: 1-146 < BRA>
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C;Species: Lycopersion featlentum (tomato)
C;Date: 24-Oct.1998 #sequence_revision 24-Oct.1998 #text_change 09-Jul-2004
C;Accession: S72492
R;Brandstaedter, J: Rossbach, C.; Theres, K.
Mol. Gen. Genet. 252, 146-154, 1996
A;Title: Expression of genes for a defensin and a proteinase inhibitor in specific areas A;Reference number: S72491; MUID:96397493; PMID:8804387
                             A;Cross-references: UNIPROT:Q8XD02; GB:AE005174; NID:912517463; PIDN:AAG58054.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-144 <GATA.
A;Cross-references: UNIPROT:Q9TZK4; EMBL:AF098987; PIDN:AAC67428.1; GSPDB:GN00020; CESP:A;Experimental source: strain Bristol N2; clone F40H3
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33494
S;Gattung, S.
submitted to the EMBL Data Library, October 1998
A;Reference number: 221358
A;Reference number: 221358
A;Reference number: 221358
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A;Introns: 39/3; 72/1; 111/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F40H3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%; Score 23; DB 2; Length 144; 100.0%; Pred. No. 2.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       23.5%; Score 23; DB 2; Le 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
A; Conservative
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F40H3.3
                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <STO>
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67 NGTF 70
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Circlession: A69883

Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Bruilleth, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, isch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, R.; M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadaie, Y.; Saro, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tamakoshi, A.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A;Authors: Yoshikawa, H.; Zummeton, E.; Yoshikawa, H.; Danchin, A.; Tata, K.; Yata, K.; Yata, K.; Yoshida, K.; Atitle: The complete genome sequence of the Grama-Dositive bacterium Bacillus subtilis.
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R;Kunst, F; Ogasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Bron, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:045478; GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13418.
A,Experimental source: strain 168
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A;Accession: A69883
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein ylyA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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A.Experimental source: shoot, cv. Moneymaker
C;Superfamily: potato proteinase inhibitor PTI
C;Keywords: serine proteinase inhibitor
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-146/Product: probable proteinase inhibitor #status predicted
F;33/Inhibitory site: Arg (trypsin) #status predicted
F;94/Inhibitory site: Arg (trypsin) #status predicted
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100.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 0;
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A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Mivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, F.; Socffone, F.; Sekiguchi, J.; Sekowska, A.; Serori akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Voshida, R.; Vamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.; A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377 translation not shown A; Molecule type: DNA A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-151 «KUN»
A; Residues: 1-151 «KUN»
A; Experimental source: strain 168
C; Genetics:
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Search completed: February 24, 2005, 15:24:26 Job time : 27.8537 secs

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Acta Virol. 38:223-228(1994).
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Bacteriophage BFK20.
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tes 7; Conserv
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Name=ORF5
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ö chlamydia t chlamydia t chlamydia t chlamydia t human immun human immun neisseria m pinus sylve neotyphodiu plasmodium uncultured uncultured MEDLINE=92381485; PubMed=1512569; Kopfiddes M., Barak I., Sisova M., Baloghova E., Ugorcakova J.; "Characterization of bacteriophage BFK20 from Brevibacterium flavum."; J. Gen. Microbiol. 138:1387-1391(1992). SEQUENCE FROM N.A.
Rablik I., Bukoveka G., Godany A., Timko J.;
"Alanlysis of the nucleotide sequence of the genome of Brevibacterium flavum CC M 251 bacteriophage BFK20.";
Chem. Zvesti 52:266-267(1998). Gaps MEDLINE-95185419; PubMed=7879712; Koptides M., Ugorcakova J., Baloghova E., Bukovska G., Timko J.; "Characterization and sequence analysis of the F2 promoter from corynephage BFK20."; ö Q9r813 Q9r816 Q9r819 Q9r8m3 Q91p2 Q991p3 Q991p4 Q70ui4 Q710f3 Q9jua3 Q9jua3 Q9jua3 Length 204; Indels Klucar L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ278322; CAB93910.1; -.
MEROPS, U35.001; -.
GO; CO006233; F:peptidase activity; IEA.
InterPro; IPR006433; Peptidase_U35.
Pfam; PF04986; Peptidase_U35, 1.
IIGRFAMS; IIGR01543; proheadase_HK97; 1. 204 AA; 22120 MW; 7B18F14718EF66E9 CRC64; Created) Last sequence update) Last annotation update) 5; Ş 30.6%; Score 30; DB .larity 29.2%; Pred. No. 25; Conservative 0; Mismatches ALIGNMENTS 204 NGTFXXXXXXXXXXXG 56 NGTFTAYASVFGNKDSYGDVVKSG 43 Q9R8L3 Q9R8L6 Q9R8L6 Q9R8N3 Q991P2 Q991P4 Q70U1A Q710F3 Q9UA3 Q7R0W6 QRASS PRT;

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Probon, PD000006, ABC transporter, 1.
SMART; SM00382; AAA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
                                                                                                        Interpro; IPR003593; AAA ATPase.
Interpro; IPR003439; ABC_transporter.
Interpro; IPR000253; FHA.
Interpro; IPR008984; SMAD FHA.
Pfam; PF00005; ABC_tran; I.
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                                 EMBL; AE000516; AAK46062.1; -.
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   laboratory
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STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
BOI=10.1128/JB.184.19.5479-5490.2002;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Hickey E.K., Kolonay J.F., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                   Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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PROSITE; PS500893; ABC_TRANSPORTER_2; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
ATP-binding; Complete proteome; Hypothetical protein.
SEQUENCE 822 AA; 87608 MW; 30747ED500ADC13F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) ABC transporter, ATP-binding protein.
                                          (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
             822 AA.
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                                                                           OrderedLocusNames=MAP3466;
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Matches 7; Conservative
             PRELIMINARY;
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                                                                Hypothetical protein.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.B., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Fellwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares S.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUR.-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE CONSERVED TRANSMEMBRANE ATP-BINDING PROTEIN ABC
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Nature 393:537-544(1998).
-!- SIMILARITY: Belongs to the ABC transporter family.
PIR; D70986; D70986.
J. Bacteriol. 184:5479-5490(2002).
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
-!- AE017232; AAS03774.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

-i- SIMILARITY: Belongs to the ABC transporter family.

EMBL; AR017239; AAS06615.1; -.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016024; F:ATP binding; IEA.

R GO; GO:000466; F:ATPs binding; IEA.

R GO; GO:000466; F:ATPs binding; IEA.

R GO; GO:000466; F:ATPs binding; IEA.

InterPro; IPR003439; AAA_ATPses.

InterPro; IPR003439; AAA_ATPses.

InterPro; IPR003439; ABC_transporter.

R Ffam; PF000498; FHA.

R Pfam; PF000498; FHA.

R Propom; PR00006; ABC_transporter; 1.

R Pfam; PF000498; FHA.

R Propom; PR00006; AAA; 1.

R PARAT; SM00342; AAA; 1.

R SMART; SM00342; AAA; 1.
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
ATP-binding; Complete proteomy
ATP-binding; Complete proteomy
SEQUENCE 873 AA; 93301 MW; 280DF91BA9B2B63F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=MAP1457;
                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                   873 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 NGTFXXXXXXXXXXXGDXXXXG 56
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=MAP3465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 29.2 nes 7; Conservative
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                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=k10;
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                                                                                                               Q73UA3
Q73UA3;
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Matches
                                          RESULT 6
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                                                                                    Q73UA3
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CA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Carnier T., Eiglmeier K., Camus J.-C., Modina N., Mansoor H.,
Carnier T., Eiglmeier K., Grondin S., Lacroix C., Monsempe C., Simon S.,
Carnier B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Carnier E., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
Carnier E., Natl. Acad. Sci. U.S.A. 100,7897-7862.
Carnier E., SimilaRity: Belongs to the ABC transporter family.
Carnier E., SimilaRity: Belongs to the ABC transporter family.
Carnier E., Carnier E.,
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 28.6%; Score 28; DB 2; Length 865; Local Similarity 29.2%; Pred. No. 3.3e+02; Pred. 7; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE CONSERVED TRANSMEMBRANE ATP-BINDING PROTEIN ABC
                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Complete proteome.
SEQUENCE 865 AA; 92152 MW; 4987186C471E47E8 CRC64;
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SEQUENCE 865 AA; 92152 MW; 4987186C471E47E8 CRC64;
                          InterPro; IPR00253; FHA.
InterPro; IPR008984; SMAD_FHA.
Pfam; PF004095; PHA; I.
ProDom; PF00498; FHA; I.
SMART; SM00340; FHA; I.
SMART; SM00240; FHA; I.
PROSITE; PS00211; ABC_TRANSPORTER 1; I.
PROSITE; PS50893; ABC_TRANSPORTER 1; I.
PROSITE; PS500893; ABC_TRANSPORTER 1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD00006; ABC transporter; 1. PROSITE; PS00211; ABC TRANSPORTER 1; 1. PROSITE; PS50093; ABC TRANSPORTER 2; 1. PROSITE; PS50006; FHA_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 NĠŤĖVNGARVDAALLHDĠĎVVTIĠ 293
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InterPro; IPR003439; ABC_transporter.
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Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
                                                                                                                                                                                                                                    MEDLINE=22225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 AA; 26355 MW; EAE4A94A64AD75C0 CRC64;
                                              OrderediocusNames=tlr1235;
Synechococcus elongatus (Thermosynechococcus elongatus
Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 AA.
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OrderedLocusNames=DP2570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 9:123-130(2002).
EMBL; AP005373; BAC08787.1; -.
InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD_FHA.
Pfam; PP00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_DOWAIN; 1.
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PubMed=15305914;
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE 246 AA
                                                                                                                           NCBI_TaxID=32046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302; Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.; "A complete sequence of the T. tengcongensis genome."; Genome Res. 12:689-700(2002).
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0
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29.2%; Pred. No. 5.8e+02;
tive 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.5%; Score 26; DB 2; Length 132; llarity 29.2%; Pred. No. 1.7e+02; Conservative 0; Mismatches 17; Indels
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Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
                                                                                                                                                                                                                                                                                      PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
ATP-binding; Complete proteome.
SEQUENCE 854 AA; 89806 MW; 4F31E633AE308BAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 AA; 15400 MW; 90936DC65A881158 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacteriaceae; Thermoanaerobacter
NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AA
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
                                         InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; AAA ATPase.
InterPro; IPR000439; FHA.
InterPro; IPR0008984; SMAD FHA.
Pfam; PF00005; ABC_tran; I.
ProDom; PD000006; ABC_tran; I.
SMART; SM00382; AAA; I.
SMART; SM00382; AAA; I.
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PROSITE; PS50006; FHA_DOMAIN; 1.
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OrderedLocusNames=TTE1969;
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InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD_FHA.
Pfam; PP00498; FHA; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 29.2 nes 7; Conservative
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Beet Local Similarity
7; Conserve
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STRAIN=CDC-1573;
PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
Fletcher L.D., Sanith R.P., Weise P., Wetherell M., Xie X.,
Zagursky R., Zhang Y., Zlotnick G.W.;
"Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2) / M145,
MEDLINE=2199410; PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=2199410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chanddra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitech B., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

Nature 417:141-147(2002).

EMBL; AL939127; CAA20163.1; -.

PIR; T34986; T34986.

HSSP; O50769; INYO.

GO; GO:0007155; P:cell adhesion; IEA.

Interpro; IRFO0782; B1943 FAS1.

Pfam; PF02466; FAS1: 11, 1.

SMART; SM00554; FAS1: 11, 1.
                                                                                                                                                                                                                                                                                 Straptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.5%; Score 25; DB 2; Length 220
26.3%; Pred. No. 5.1e+02;
tive 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 AA; 22362 MW; 78C08D7932B12C32 CRC64;
                                                                                                                                                                                               Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Lipoprotein (Fragment).
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                         95 NGTFNAKEVYITGTLGSGNAARTG 118
                                                                                                                                                                             Created)
                                                                                                                                 PRT;
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                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25, Putative secreted protein.
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Best Local Similarity 26.33
Matches 5; Conservative
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                                                                                                                                                                                                                                                               ORFNames=SC4A2.11c;
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[1] **.
SEQUENCE FROM N.A.
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                                                                                                                                                      086667;
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086667
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MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 1361:743-749(2003).

EMBL, AP005078; BAC59897.1; -.

Complete proteome; Hypothetical protein.

SEQUENCE 598 AA; 64664 MW; 3C41591D8AE218A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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BMBL: AF28B477; AAQ14336.1; -.
GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Feng S., Hodzic E., Kendall L.V., Smith A., Freet K., Barthold S.W.;
"Cloning and expression of a Helicobacter bilis immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
Vibri TaxID=670;
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InterPro; IPR004311; Put vacuo_cyttox.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03077; VacA2; 1.
SEQUENCE 1543 AA; 167034 MW; 6CADA242FFF4297E CRC64;
                                                                                                                                                                                               Last sequence update)
Last annotation update)
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C5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                               598 AA
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                                                                                                                                                                             Created)
                                                                                                                                 PRT;
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187 NGTFVAGKKITFAELRSGD 205
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                                                                                                                                                                   01-JTM-2003 (TrEMBLrel. 24, 0
01-JTM-2003 (TrEMBLrel. 24, 1
01-JTM-2003 (TrEMBLrel. 24, 1
Hypothetical protein V91594.
OrderedLocusNames=VP1594;
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Best Local Similarity 25.0.
Local 6; Conservative
                                                                                                                               PRELIMINARY;
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Query Match

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Length 220;

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STRAIN=JS3001;
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J. Bacteriol. 184:2709-2718 (2002).
EMBL, AF193064; AAF07961.1; -. SEQUENCE 359 AA; 35434 MW; 62CA79A902F4B961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Umelo-Njaka E., Bingle W.H., Borchani F., Le K.D., Awram P., Blake T., Nomellini J.F., Smit J.,
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter. (Caulobacter.) (CBI_TaxID=155892;
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                                                                                                                                                                                                    25.5%; Score 25; DB 2; Length 260; 25.0%; Pred. No. 6e+02;
                                                                                                                                                                                                                                                                 18; Indels
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260 lipoprotein.
27563 MW; 8CC49D53851B635F CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21972786; PubMed=11976300;
DOI=10.1128/JB.184.10.2709-2718.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 NDTFVAGEVAGAATLTVGDTLSGG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 NGTFXXXXXXXXXXXGDXXXXG 56
                                                                                                                                                                                                                                                                                                                          33 NGTFXXXXXXXXXXXGDXXXXG 56
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                                                                                                                                                                                                                                                                                                                                                                              NGTLTLSAQGAEKTYGNGDSLNTG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
Infect. Immun. 72:2088-2100(2004)
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NCBI_TaxID=155892;
                              EMBL; AY330406; AAR84481.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Truncated S-layer protein.
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les 6; Conservative
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                                                                                                                                           260 AA;
                                                                                                                                                                                                                                Local Similarity
les 6; Conserv
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                                                         Lipoprotein.
NON TER
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SLAP_CAUCR
ID SLAP_CAUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=rsaA;
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                       Query Match
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                                                                                                                   CHAIN
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CORNALI
LD CORNALI
DT 01-MA
D
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAINS-ATCC 19089 / CB15;

STRAINS-21170568; Dubmed-11259647; DOI=10.1073/pnas.061029298;

MEDLINE-211705698; Dubmed-11259647; DOI=10.1073/pnas.061029298;

Nicrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Podson R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermoleeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Bingle W.H., Awram P.A., Nomellini J.F., Smit J.K.;
"The secretion signal of C. crescentus S-layer protein is located in the C-terminal 82 amino acids of the molecule.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=89008089; PubMed=3049545;
Fisher J.A., Smit J.K., Agabian N.;
"Transcriptional analysis of the major surface array gene of
                                                                                                                                                                              Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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STRAIN=ATCC 19089 / CB15;
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Calcium-binding; Cell wall; Complete proteome;
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EMBL; AF193063; AAF19365.1; -.
EMBL; AE005779; AAK22991.1; ALT_INIT.
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InterPro; IPR011049; Serralysn_like_C
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INIT MET 0 0 SEQUENCE 1025 AA; 98001 MW; AD7.
[2]
REVISIONS TO 376; 636 AND 842-843.
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TIGR; CC1007; -.
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Thiamine biosynthesis protein This.
Name=this; ORFNames=BPSL3153;
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                                                                                                                                                                                                                                                                                               5; Conservative
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nes 5; Conserv
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Best Local Similarity
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SEQUENCE FROM N.A.
                     STRAIN=ATCC 23344;
SEQUENCE FROM N.A.
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01-OCT-2000
01-MAR-2003
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Q9KHW4;
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ID O9
AC O9
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

REMBL: A662281; Cartiform of the control of
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Saccharomycetales; Saccharomycetaceae; Pichia.
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Burkholderia mallei ATCC 23344.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=243160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.5%; Score 25; DB 2; Length 1105; 26.1%; Pred. No. 2.4e+03; Live 0; Mismatches 17; Indels
               Query Match 25.5%; Score 25; DB 1; Length 1025; Best Local Similarity 25.0%; Pred. No. 2.2e+03; Matches 6; Conservative 0; Mismatches 18; Indels
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SEQUENCE 1105 AA; 122926 MW; 4878904DF7ECF50A CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Thiamine biosynthesis protein This, putative.
                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                        33 NGTFXXXXXXXXXXXGDXXXXG 56
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Pfam; PP00690; Cation ATPase N; 1:
Pfam; PP00122; B1-E2 ATPase; 1.
Pfam; PP00702; Hydrolase; 1.
PRINTS; PR001121; NAKATPASE.
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                                                                                                                                                                                                                                                                                                                                                       Pichia farinosa (Yeast).
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                                                                                                                                                                                                                                                                                                                P-type ATPase.
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062GC5
AC 062GC
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DT 25-0C
DT 25-0C
DT 25-0C
DR Thiam
GN Burkh
OC Bacte
OC Burkh
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Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
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Anderson M., Moule S., Price C., Quail M.A.,
Mhitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
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T. Genomic plasticity of the causative agent of melioidosis,
T. Burkholderia pseudomallei.";
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B. BMBL, BX571965; CAH371631.1;
S. BGUENCE 65 AA; 6572 MW; 5364B131908DARFE CRC64;
Nickman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T., Ulrich R.L., Ronning C.M., Brinkec L.M., Daugherty S.C., Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Skructural flexibility in the Burkholderia mallei genome."; "Structural flexibility in the Burkholderia mallei genome."; EMBL, CP000010; Au148294.1; "EMBL, CP000010; Au148294.1; "S64B111908DABFE CRC64;
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Burkholderiaceae, Burkholderia.
NCBI_TaxID=272560;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Bakkan D., Brooks K.D., Thomson N.R., Pickard D., Waker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
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Romplete genome sequence of a multiple drug resistant Salmonella
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T. Mature 413:498-852(2001).
B. EMBL, ARC18001, AAC38069.1;
T. Remil, AL627282; CAD09328.1;
T. InterPro; IPR007001, Shufflon N.
Remil, AL627282; CAD09328.1;
T. Remil, Parkell Shufflon N.
Remil, Prodence
Sequence Protecome.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Pubmad=14688076; DOI=10.1128/IAI.72.1.22-28.2004;
Tam C.K.P., Hackett J., Morris C.;
"Salmonella enterica serovar Paratyphi C carries an inactive
                                                                                                                                                                                                                                                                                                                                         24.5%; Score 24; DB 2; Length 435; 25.0%; Pred. No. 1.8e+03; ive 0; Mismatches 18; Indels
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Local Similarity 25.0%; Pred. No. 1.9e+03;
les 6; Conservative 0; Mismatches 18; Indels
 MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
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EMBL; AY249242; AAP83041.1; -.
InterPro; IPR071001; Shufflon.N.
Pfam; PF04917; Shufflon.N; 123098601189B5F6 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Transferrin binding protein B subunit (Fragment).
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Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                 STRAIN=Serovar Dublin,
MEDLINE=2934313; PubMed=14580391; DOI=10.1016/j.micpath.2003.08.001;
MEDLINE=29343013; PubMed=14580391; DOI=10.1016/j.micpath.2003.08.001;
MORTIS C., Tam C.K.P., PubMed=1118 T.S., Jones P.W., Hackett J.;
"Salmonella enterica serovar Dublin strains which are Vi antigen-positive use type 1VB pili for bacterial self-association and human intestinal cell entry.";
Microb. Pathog. 35:279-284(2003).
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MEDLINE=98087429; PubMed=9427557; DOI=10.1016/S0378-1119(97)00466-6;
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                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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"Molecular cloning, nucleotide sequence, and function of a site-
specific recombinase encoded in the major 'pathogenicity island'
Salmonella typhi.";
Gene 202:139-146(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 434;
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STRAIN=servoar Dublin;
Morise C.J., Hackett J.;
Submitted (NAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF247502; AAF81218.1; -.
InterPro; IPR07001; Shufflon.N.
Pfam; PF04917; Shufflon N; 1.
SEQUENCE 434 AA; 46136 MW; 0273A4153BDD3518 CRC64;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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25.0%; Pred. No. 1.8e+03;
live 0; Mismatches 18;
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; Pubmed=12644504;
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Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal Neisseriae
and Neisseria meningitidis.";
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Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal Neisseriae
                                                                                                                                                                                               MEDLINE-1221(108) PubMed=11287631; DOI=10.1073/pnas.061386098;
Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L.,
Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S.,
Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.;
"Fit genotypes and escape variants of subgroup III Neisseria
meningitidis during three pandemics of epidemic meningitis.";
EMBL; AJ276928; CAC21592.1;
CG; GG:0016020; C:membrane; IEA.

GG; GG:0004998; F:transferrin receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21221108; PubMed=11287631; DOI=10.1073/pnas.061386098; Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L., Popovic T., Schuurman I.G.A., Adegbola R.A., Zuthh K., Gagneux S., Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.; Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis."; Proc. Natl. Acad. Sci. U.S.A., 98:5234-5239(2001).
GO; GO:0016020; Camembrane; IEA.
GO; GO:0004998; F:transferrin receptor activity; IEA.
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Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Neisseriaceae, Neisseria.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Transferrin binding protein B subunit (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last seq
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                                            NCBI_TaxID=487;
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                                                                                STRAIN=21500;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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MEDLINE=20305048; PubMed=10844690;
Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal Neisseriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21221108; PubMed=11287631; DOI=10.1073/pnas.061386098; MEDLINE-21221108; PubMed=11287631; DOI=10.1073/pnas.061386098; MEDLINE-21221108; PubMed=11287631; DOI=10.1073/pnas.061386098; Popovic T., Schuurman I.G.A., Adegbola R.A., Zutth K., Gagneux S., Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.; Pit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis."; Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).

BMBL, A0276927; CAC1591.1; ---
GO: GO:0004998; F:transferrin receptor activity; IEA.
                                                                                                                                              Gaps
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Transferrin-binding protein 2 precursor (TBP-2).
Name=tbpB, Synonyms=tbp2; OrderedLocusNames=NWA2025;
Neisseria meniagitidis (Serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                               Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.5%; Score 24; DB 2; Length 686; 25.0%; Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                              684 AA; 73610 MW; 13D6B69FBDC5A425 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Transferrin binding protein B subunit (Fragment).
                                                                                             24.5%; Score 24; DB 2; 1
25.0%; Pred. No. 2.7e+03;
                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        698 AA
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                                                                                                                                                                                                                                           576 NĠTLTADNRQAATFTIVĠĎIEGNĠ 599
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                                                                                                                                                                                          33 NGTFXXXXXXXXXXXG 56
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                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 36:1049-1058(2000).
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Pfam; PF01298; Lipoprotein_5; 1.
NON TER
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Best Local Similarity 25.09
Matches 6; Conservative
                                                                                                                                              Conservative
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                                                                Query Match
Best Local Similarity
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MEDITRE=2231233; PubMed=12033788; DOI=10.1006/viro.2002.1408;
Chuchird N., Nishida K., Kawasaki T., Fujie M., Usami S., Yamada T.;
A variable region on the chlorovirus CVK2 genome contains five copies of the gene for Vp260, a viral-surface glycoprotein.";
Virology 295:289-298(2002).
EMBL; AB063108; BAB83469-1; -.
Pfam; PP60598; Chlorovi GP Frt; 14.
SEQUENCE 1464 AA; 149988 MW; ECCDA711437B6F5D CRC64;
                                                                                                                                                                                                                               Linz B., Schenker M., Achtman M.; "Frequent interspecific genetic exchange between commensal Neisseriae and Neisseria meningitidis." Mol. Microbiol. 36:1049-1058(2000).
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AND STATE A
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             699 AA; 75373 MW; 60B6F8CECA208ADE CRC64;
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Last annotation update)
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Pred. No. 5.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 NGTFXXXXXXXXXXXGDXXXXG 56
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                                                                                                                                                                                                   MEDLINE=20305048; PubMed=10844690;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 NGTFXXXXXXXXXX
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    Neisseriaceae; Neisseria
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                        WCBI_TaxID=487;
                                                                                                                                                          STRAIN=25642;
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Q57226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Lipoprotein; Outer membrane; Palmitate; Receptor;
                                                                                                                                                                                                                                                                        "Human antibody responses to A and C capsular polysaccharides, IgAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=20222565 PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher, C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamiln N., Holroyd &
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Slmmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 20 By similarity.
21 698 Transferrin-binding protein 2.
21 21 N-palmitoyl cysteine (Probable).
21 S-diacylglycerol cysteine (Probable) 698 AA; 75176 MW; 83FBE14DDF617B1F CRC64;
                                                                                                                                                                                                                                                                                                         protease and transferrin-binding protein complex stimulated by infection with Neisseria meningitidis of subgroup IV-1 or ET-37
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Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                      STRAIN=Z2491 / Serogroup A / Serotype 4A;
Brieske N., Quentin-Millet M.-J., Schenker M., Schnibbe T.,
Achtman M.;
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Transferrin binding protein B subunit (Fragment).
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25.0%;
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Nature 404:502-506(2000).
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                                    NCBI_TaxID=65699;
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Chlamydia trachomatis.
Bacteria, Chlamydiae; Chlamydiales, Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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                                                        FYRAIN-B2f;
Hsieh Y.-H., Bobo L.D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF070284; AAC25254.1; -.
NON TER 1 2 2
NON TER 22 22
SEQÜENCE 22 AA; 2425 MW; B102482844167521 CRC64;
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HBieb Y. T. H., Bobo L.D.;
Submitted (UNN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF070276; AAC25246.1;
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Haish Y.-H., Bobo L.D.;
Submitted (UNN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF070272; AAC25242.1; -
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Major outer membrane protein (Fragment).
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Last annotation update)
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Pred. No. 1.8e+02;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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SEQUENCE FROM N.A.
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Q9R8L6;
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Q9R8L6
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Benbli, S77984; AAB34697.1; -.
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"DNA sequence polymorphism of the Chlamydia trachomatis ompl gene.";
J. Infect. Dis. 168:1225-1230(1993).
BEMBL; S66728; AAB28611.1; -.
NON TER 22 22
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Chlamydia trachomatis.
Bacteria: Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                           Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Major outer membrane protein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence
01-JUNY-2001 (TEMBLrel. 17, Last annotat.
Major outer membrane protein (Fragment).
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MEDLINE=94044912; PubMed=7901288;
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SEQUENCE FROM N.A.

MEDLINE=21109142; PubMed=11162839; DOI=10.1006/viro.2000.0753;
A Gleazi S., Menzo. S., Brambilla A., Panina Bordignon P., Lorini A.L.,
Clementi M., Poli G., Vicenzi E.;
T Inhibition of R5X4 dualtropic HIV-1 primary isolates by single
T chemokine co-receptor ligands.";
Virology 280:553-261(2001).
R GGJ GO:0016021; C:integral to membrane; IEA.
R GGJ GO:0019031; C:integral to membrane; IEA.
GGJ GO:0019031; C:viral envelope; IEA.
R GGJ GO:0005198; F:structural molecule activity; IEA.
R GGJ GO:0005198; F:structural molecule activity; IEA.
R HO GO: GO:0005198; F:structural molecule activity; IEA.
R HO GO: GO:005198; F:structural molecule activity; IEA.
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Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
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NON TER 31 31
SEQUENCE 31 AA; 3396 MW; 1FE12AAOF6C50B9A CRC64;
                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein V4 region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                     Major outer membrane protein (Fragment)
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Best Local Similarity
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24 NGTF 27
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Q991P3;
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Q991P3
ID Q991P
AC Q991P
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Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia.
NCBI_TaxID=813;
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Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia.
NCBI_TaxID=813;
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF070248; AAC25218.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-B2d;
Hrich Y.-H., Bobo L.D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF070268; AAC25238.1; -.
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22 AA; 2425 MW; B102482844167521 CRC64;
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            Pred. No. 1.8e+02;
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100.0%; Pred. ...
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
U-MAY-2000 (TrEMBLrel. 13, Last annotati
Major outer membrane protein (Fragment)
Name=omp-1;
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Best Local Similarity 100...
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أحم 4; Conservative
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               Best Local Similarity
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NGTF 13
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ID Q9R8N3
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QORBLE
QORBLE
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Search completed: February 24, 2005, 15:23:35 Job time : 113.715 secs
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A Ghezzi S., Menzo S., Brambilla A., Panina Bordignon P., Lorini A.L.,
Clementi M., Poli G., Vicenzi E.;
Tinhibition of RX4 dualtropic HIV-1 primary isolates by single
T chemokine co-receptor ligands.";
Virology 280:253-261(2001).
MEMBL, AR33321; AAK2196.1;
MEMBL, AR33221; Cintegral to membrane; IEA.
GO; GO:0019028; Civiral capsid; IEA.
GO; GO:0019028; Civiral envelope; IEA.
GO; GO:0019028; Fistructural molecule activity; IEA.
InterPro; IPR0031; Girls envelope IEA.
MEMBL, PR00516; GP120;
MEMBL, PR00516; GP
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MEDIJIRE=21109142; PubMed=11162839; DOI=10.1006/viro.2000.0753;
MEDIJIRE=21109142; S., Bendellia A., Panina Bordignon P., Lorini A.L.,
Clementi M., Poli G., Vicenzi E.;
"Inhibition of RS44 dualtropic HIV-1 primary isolates by single
chemokine co-receptor ligands.";
Virology 280:253-261(201)
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Pred. No. 2.6e+02;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019021; C:integral to membrane; IEA.
GO; GO:0019011; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
INTERPRO; IRRONO777; GP120.
AIDS; Coat protein; Envelope protein; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 AA; 3395 MW; EF412AA0F6C50B97 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein V4 region (Fragment).
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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V 100.0%; Pred. No. ...
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Matches 4; Conserv
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SEQUENCE
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0991P4
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"Diversity of laccase genes from basidiomycetes in a forest soil.";
Soil Biol. Biochem. 36:1025-1036 (2004).
BMBL; AJ540279; CAD62542.1;
BSSP; Q97780; 1A65.
GO; GO:0008471; F:laccase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
Oxidoreductase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                uncultured basidiomycete.
Bukaryota, Fungi; Basidiomycota, environmental samples.
NCBI_TaxID=175244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 42 AA; 5033 MW; 4381115F42638C25 CRC64;
               070UI4;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Laccage (EC 1.10.3.2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.5%; Score 23; DB 2; Le
100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0;
  PRT;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 4 2
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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February 24, 2005, 15:03:10; Search time 140.537 Seconds (without alignments) 184.386 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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67 US-09-936-956-19 336 1 WIFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDEITVG Title: Perfect score: Sequence:

Scoring table:

2105692 segs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:* geneseqp2003as:*geneseqp2003bs:* A_Geneseq_16Dec04: geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abp54942 Saccharom Abr53872 Protein s Abu61612 Yeast SPK Adk64880 Disease t Disease t Candida a Candida a Bacterial Bacterial Pseudomon C glutami Mycobacte Mycobacte Human nov Human nov pro pro aci Chf Aaw73894 Yeast MEC Aaw26664 Yeast che dia cel Human Novel Human Human Human Human Human Human Amino Human Description Abp73798 Ads44244 Adn19646 Abo68456 Aau15856 Abu54925 Abm83354 Abm83354 Abm83352 1 Aab93182 1 Abb97233 1 Aag89798 Aaw32352 Aaw32420 Aab83843 Aab20219 Aab03445 SUMMARIES ABR53872 ABU61612 ADK64880 ABM83353 ABM83352 AAB93182 AAB03445 ABP73798 ADS44244 ADN19646 AB068456 AAU15856 ABU54925 ABM83354 AAG89798 AAW32352 AAW32420 ABP54942 В Length Query Score Result Š

Σ.	Aay38957 M. tuberc Aay39094 M. tuberc	Aaw72886 Mycobacte	Mycoba	Aam48994 Human Chk	Adl32563 Human Chk	Aag68375 Human Chk	Aay06204 Human che	Novel	Human	Aam48995 Human Chk	Human (Adl32561 Human Chk	Adm72213 Human TAS	Ado44010 Amino aci	Adq09232 Human CHE	Adn61455 Human KPP
AAW64292 AAW81655	AAY38957 AAY39094	AAW72886 AAY21903	AAM50735	AAM48994	ADL32563	AAG68375	AAY06204	AAY05765	AAM48996	AAM48995	ABG30701	ADL32561	ADM72213	ADO44010	ADQ09232	ADN61455
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148	148	161	163	514	514	543	54	543	54	54.	543	543	54	543	54.	286
23.7	23.7	23.7	23.7	22.9	22.9	22.9	6.2	22.9	6.2	22.9	22.9	6.2	5.9	22.9	6.2	5.9
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79.5	79.5	79.5	79.5	77	77	77	77	77	77	77	77	77	77	77	77	11
26	7 7 8 7 8 8	30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

cycle checkpoint gene; yeast; radiation resistance; detection; Weinert TA; UNIV ARIZONA.
HUTCHINSON CANCER RES CENT FRED AAW73894 standard; protein; 776 AA 92US-00882051. 92US-00884426. 93WO-US004458. 94US-00198446. 97US-00870693. Yeast MEC2 protein sequence (first entry) Saccharomyces cerevisiae (UNIW) UNIV WASHINGTON. Cell cycle check G2/M checkpoint 14-MAY-1992; 12-MAY-1993; 18-FEB-1994; 06-JUN-1997; 12-MAY-1992; 08-APR-1999 US5866338-A. 02-FEB-1999 AAW73894; (UYAR-) (HUTC-) RESULT 1 AAW73894

Plon SE, Groudine MT, Hartwell LH,

WPI; 1999-141919/12. N-PSDB; AAX01275.

Nucleotide sequences that hybridise to huRAD cDNA - method for isolating human checkpoint cDNA, and antibody to CDC34.

Example 4; Col 89-96; 73pp; English.

This sequence is the yeast MEC2 protein. The DNA encoding this sequence is necessary for \$2/M cell cycle checkpoint control. This sequence was identified using the method of the invention for isolating a human checkpoint cDNA that is capable of restoring growth at a restrictive temperature in a yeast test cell, where the yeast test cell comprises a genome having a first gene that forms a DNA strand break at a restrictive temperature and a second gene that fails to induce a cell cycle arrest in response to the DNA strand break, whereby the growth of the yeast test

Example 4; Col 85-90; 54pp; English.

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cell is inhibited at the restrictive temperature, comprising: (a) obtaining a human cDNA library comprising several human cDNA clones individually into plasmid vectors containing a selectable marker gene; (c) transforming a culture of the yeast test cells with the plasmid vectors from the preceding step; (d) selecting for yeast test cells transformed with the selectable marker gene; (e) growing the selected transformed with the selectable marker temperature and isolating a candidate transformant capable of growing at the restrictive temperature; and (f) identifying the human cDNA carried by the candidate cransformant and determining that the human cDNA arried by the candidate transformant and determining that the human cDNA is less than 50% homologous with both the first gene and the human cDNA is less than 50% homologous with both the first gene and than the property of the proper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGGKVEKNSNQLLS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 313.5; DB 2; Length 776;
Pred. No. 2.4e-33;
0; Mismatches 6; Indels 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast checkpoint control protein MEC2.
                                                                                                                                                                                                                                                                                                                     confer radiation resistance on a cell
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93WO-US004458.
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89.7%;
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Best Local Similarity
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25-FEB-1998
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12-MAY-1993;
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This protein is encoded by novel yeast checkpoint control gene MEC2 (see AAT91040). Yeast checkpoint control genes RAD17, RAD24, MEC1, MEC2 and AAT91040). Yeast checkpoint control genes RAD17, RAD24, MEC1, MEC2 and MEC3 (AAT91037-41, respectively) are responsible for recognising if the cell has suffered DNA damage in the form of radiation or chemical damage or if the cell has failed to complete DNA replication because of chemical inhibition or intrinsic error. Upon recognising damage or failure, the genes are responsible for inhibiting mitosis. The purpose of this checkpoint control is that it preserves the viability of the cell and the integrity of the genome by providing the cell time to repair these cinsults prior to undertaking mitosis. The genes are potentially useful in developing cancer chemotherapeutics, cancer chemoprevention agents, and environmental toxicology tests. They can be used to produce proteins (see AAM26661-65) that can then be screened for chemical agents that would interfere with checkpoint controls. Cloned genes can also be used to develop yeast strains in which these genes are deleted. Such yeast strains can then be used to find the homologous human genes (see AAT91034 516). (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Score 313.5; DB 2; Length 821; 89.7%; Pred. No. 2.6e-33; ive 0; Mismatches 6; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP54942 standard; peptide; 821 AA.
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|26 QGDEITVG 133
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N-PSDB; ABV73988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 QGDEITVG
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 821 AA;
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Matches
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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC6010-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful
The present sequence is the protein sequence of Saccharomyces cerevisiae PSFX1, a protein related to human tyrosine threomine kinase (TTK, see ABP5438). TTK polymucleotides and polypeptides of the invention encompass polymucleotides and polypeptides having sequence similarity or esquence identity to human TTK and other genes and gene products related to TTK, such as SPK1. The invention is based on the finding that TTK is differentially expressed in various forms of cancer. It provides methods colon cancer cells, by detection of expression levels of TTK, as well as diagnostic, prognostic and therapeutic methods. These methods can be used as the basis of rational therapy. Assays for identifying molecules that modulate the activity of these genes in cancers, as well as methods of inhibiting tumour growth by inhibiting the activity of TTK are also
                                                                                                                                                                                                                                                                                                                                                                                                66 WIFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTWGTWLNGQKVEKNSNQLLS 125
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                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuester BD;
                                                                                                                                                                                                                                                                                                       Score 313.5; DB 5; Length 821;
Pred. No. 2.6e-33;
0; Mismatches 6; Indels 1;
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Superti-Furga GD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein sequence #SEQ ID 2609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2001; 2001EP-00130253
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89.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marzioch M, Schultz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                        61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CELL-) CELLZOME AG
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGDEITVG
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                                                                                                                                                                                                                                                                      Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1258494-A1
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                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                        Best Local
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a subject, comprising comparing the expression levels of tyrosine threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or polynchototide in a test cell obtained from the subject and in a normal non-cancer cell, where an increase in the expression level of TTK protein or nucleic acid in the test cell compared to that in the normal cell, and in the test cell compared to that in the normal cell, are reducing growth of a cancerous cell (by contacting a cancerous cell with an amount of an agent effective to reduce TTK polypeptide activity in the cell), an assay for identifying a candidate agent that reduces growth of a cancerous cell (TTK polypeptide activity of a TTK polypeptide in the presence of a candidate agent; and (ii) comparing
for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                66 WIFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVERNSNQLLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting cancer in a subject, by comparing expression levels of tyrosine threonine kinase polypeptide or polymucleotide in a subject cell and a normal cell, where an increase in the expression level in the test cell is indicative of cancer.
                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to detecting cancer (other than ovarian cancer) in
                                                                                                                                                                                                                            1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                           Gaps
                                                                                                                                                                                        1;
                                                                                                                                                       Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast, tyrosine threonine kinase, TTK; cancer, cytostatic, mitotic checkpoint gene; SPK1.
                                                                                                                                                                                         Indels
                                                                                                                                                     Score 313.5; DB 6;
Pred. No. 2.6e-33;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 30-32; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chan VW;
                                                                                                                                                                                                                                                                                                                                                                                                                         ġ
                                                                                                                                                                                                                                                                                                                                                                                                                       ABU61612 standard; protein; 821
                                                                                                                                                         93.3%;
89.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-2001; 2001US-0289813P.
                                                                                                                                     Query Match
Best Local Similarity 8>....
Best Good Similarity 8>....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                 OCDELTVG 133
                                                                                                                                                                                                                                                                                                QGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REIN/) REINHARD C.
(JEFF/) JEFFERSON A
(CHAN/) CHAN V W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-456566/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast SPK1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACA62264.
                                                                                                                        Sequence 821 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU61612;
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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).

Disclosure; SEQ ID NO 3151; 13pp; English.

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the activity of TTK polypeptide in the presence of a candidate agent relative to TTK polypeptide activity in the absence of the candidate agent, identifying an agent that reduces TTK activity (comprising: (i) contacting a cancerous call displaying elevated expression of a TTK-encoding polynucleotide with a candidate agent; and (ii) determining the effect of the candidate agent on TTK polypeptide activity) and assessing the prognosis of a cancerous disease other than ovarian cancer in a subject (comprising: (i) detecting expression of TTK -encoding comparing a comparisation of TTK-encoding polynucleotide in the test cancer cell of expression of TTK-encoding polynucleotide in the test cancer cell with a level of expression of the polynucleotide in a control noncarcer cell, where the level of expression of TTK in the test cancer cell with a level of expression of TTK in the centrol noncarcer cell, where the level of expression of TTK in the cancer cell is indicative of the prognosis of the cancercus disease). The methods are cellulative of the prognosis of the cancercus disease). The methods are reducing growth of cancercus cells, identifying a candidate agent that reduces TTK activity and assessing the prognosis of a cancercus disease other than concert. The methods are also useful for determining the ability of a subject to respond to a particular therapy e.g. as a basis of rational therapy. The present sequence represents a closely related compared to prognosis of a subject is the prognosis of a cancercus and a cancercus of a subject to respond to a particular therapy e.g. as a basis of protein to human TTK, in this case yeast SPKI (not defined)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
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0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.3%; Score 313.5;
89.7%; Pred. No. 2.6
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Best Local Similarity 89.7
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1338608-A2.
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66 WIFGRNPACDYHLGNISRLSNRHFQILLGEDGNLLLNDISTNGTWLNGQKVERNSNQLLS 125

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1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS

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Gaps

1;

Length 821; Indels

Score 313.5; DB 7; Pred. No. 2.6e-33; 0; Mismatches 6;

Query Match 93.3%; Best Local Similarity 89.7%; Matches 61; Conservative

Sequence 821 AA;

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Growth inhibition; survival; pathogen; fungal infection; vulvovaginitis.
                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid molecule and polypeptides essential for survival and growth of yeast candida albicans useful for treating candida albicans associated diseases and for identifying antifungal compounds.
                                                                                                                                                                                                                                                                                                De Backer MD, Luyten WHML, Viaene JE;
                                                                                               Candida albicans essential growth protein #3.
                       AAB03445 standard; protein; 699 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 16; 112pp; English.
                                                                                                                                                                                                                         99WO-EP009833.
                                                                                                                                                                                                                                                98EP-00204122
                                                                                                                                                                                                                                                                                                Contreras RH, Nelissen B,
Logghe MG, Vialard JE;
                                                                       03-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                       (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                    WPI; 2000-431302/37.
                                                                                                                                               Candida albicans
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA52791
                                                                                                                                                                        WO200034481-A2.
                                                                                                                                                                                                                                                04-DEC-1998;
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                                                                                                                                                                                               15-JUN-2000
                                                                                                                                                                                                                                                                                                             Logghe MG,
                                               AAB03445;
RESULT
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New proteins and protein complexes from eukaryotes, useful as targets in diagnosing or screening, or in diagnosing or screening for the presence of a disease or discret, or a predisposition for developing a disease or disorder in a subject.

Gavin A, Superti-Furga G, Kuester B, Schultz J;
4, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
Leutwein C, Rick J;

M, Grandi P, , Leutwein C,

Michon A, Bauer A, Marzioch

WPI; 2003-638460/61. N-PSDB; ADK64881

20-DEC-2001; 2001EP-00130253

(CELL-) CELLZOME AG.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene
The present sequence is a protein which is essential for the survival and growth of Candida albicans. This fungus causes infection, such as vulvovaginitis, in humans, particularly in those who are immunocompromised. The protein and its gene can be used to diagnose infection, and they can be used as targets for inhibiting the proliferation of the fungus. This protein and gene are particularly useful as they are thought to be species-specific
                                                                                                                                                                                           Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                            1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXL-LNDISINGTWLNGQKVEKNSNQLL
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Fungus, yeast, tetracyclin, promoter, GRACE strain, biosynthesis,
signal transduction, DNA replication, cell division, growth,
proliferation, Candida albicans, fungicide, antifungal.
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                                                                                                                          50.0%; Score 168; DB 3; Length 699; 53.6%; Pred. No. 1.4e-13; ive 8; Mismatches 22; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans essential protein SEQ ID NO 7635.
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                                                                                                                                                                                                                                                                                                                     ABP73798 standard; protein; 699 AA
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                      Local Similarity 53.6 hes 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-566694/60.
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                                                                                                    Sequence 699
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                                                                                                                           Query Match
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that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (Mi) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans calls and for treating infection by C. albicans. The present sequence is that of an essential candida ablicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXL-LNDISTNGTWLNGOKVEKNSNQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 168; DB 5; Length 699; 53.6%; Pred. No. 1.4e-13; cive 8; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADS44244 Btandard; protein; 609 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial polypeptide #22674.
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nes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 NOGDETAVG 130
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SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 SQGDEITVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 699 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003233675-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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(SLAT/)
(CHEN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant as a crop plant such as maize or soybean. The method of producing a transformed plant the such as maize or soybean. The method of producing a plant is a crop plant such as maize or soybean. The method of producing a plant with the naving an improved property comprises transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of combination improved ylath by modification of carbohydrate, nitrogen or property property in property in property property property property plant property plant growth regulators, increased rate of content, improved ylath by modification of carbohydrate, nitrogen or property property plant property plant property plant property plant property plant property plant growth regulators, increased rate of content, improved ylath by modification of carbohydrate, nitrogen or property property plant property plant plant property plant plant property plant plant property plant property plant pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   providing improved plant growth and development under at least one stress condition, improved lighin production or improved galactomannan production. This sequence represents a bacterial polypoptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 RNDSDESENVVFLHGKSKGLKNLLKSSASSTFSNNFRHSSNGTFLNFVSESLIRLQFTDV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----STNGTWLN------ 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; acond tolerance; neat tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WIFGRNPACDYHLGNISRLSNKHFQI------LXXXXXXLLNDI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.7%; Score 93; DB 8; Length 609; 23.2%; Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   format from USPTO at seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: ||| :|| :|
179 IXERLAKNSRTILSNGDEIRIG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 -GOKVEKNSNOLLSOGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN19646 standard; protein; 474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-2003; 2003US-00369493.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 609 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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ADN19646
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention aloc relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the cardinant DNA construct and growing the transformed plant with the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved jield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by production, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the
                                                                                                                                                                                                                      New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GRSNTCNYQLLQFT-ASYKHFRVYSVLIDDDMDPLVYCEDQSSNGTFLNHRLIGKGNSVL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLN-----DISTNGTWLNGQKVEKNSNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%; Score 86.5; DB 8; Length 474; 33.3%; Pred. No. 0.01; ive 14; Mismatches 25; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at segdata.uspto.gov/sequence.html.
                                                                                                                                    Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa polypeptide #631.
                                                                                                                                  Chen X,
                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2299; 122pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO68456 standard; protein; 558 AA.
                                                                                                                                  Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 33.38
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 LSDGDILDV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S8 LSQGDEITV 66
CAO Y.
HINKLE G J.
SLATER S C.
                                                                                       GOLDMAN B S
                                                                                                                                                                           WPI; 2004-061375/06
                                                                                                                                  Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 474 AA;
                                                                   CHEN X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6551795-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
  CAOY/)
                                                                                     (GOLD/)
                                                                   (CHEN/)
                        HINK/)
                                             SLAT/)
                                                                                                                                  Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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2000US-0235836P
WO200155322-A2
                         02-AUG-2001
The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and theraphylaxis and treatment of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a companylaxis and treatment of pathological conditions resulting from a companylaxis and treatment of pathological conditions resulting from a companient infection, for evaluating a compound, such as a polypeptide, components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of pseudomonas species using biochip technology. Sequences or other sequences of Pseudomonas species using biochip technology. Sequence absorbance and sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rhematoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; Alzheimer's disease; infection; ocular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 TIGRGPDNDWVLPDPERLVSSRHCTILNRDGVYYLTDTSTNGVLLVNAGHRLRRGNSEPL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFGRNPACDYHLGNISRL-SNKHFQILXXXXXXLLNDISTNGTWL--NGOKVEKNSNQLL 58
                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment opathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%; Score 85.5; DB 7; Length 558;
33.3%; Pred. No. 0.017;
tive 13; Mismatches 30; Indels 3; Gaps
                                                                                                 Bush D;
                                                                                                                                                                                                             Disclosure; SEQ ID NO 17202; 455pp; English.
                                                                                              Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human novel secreted protein, Seg ID 809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU15856 standard; protein; 426 AA
                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                   seqdata.uspto.gov/sequence.html
             99US-00252991.
                                   98US-0074788P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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152 QDGETVRLG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOGDEITVG 67
                                                                                                                        WPI; 2003-615309/58.
N-PSDB; ABD02027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 558 AA;
           18-FEB-1999;
                                  18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001
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2000US-0217487P.
2000US-0217496P.
2000US-0218290P.
17-JAN-2001; 2001WO-US001341
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29-SEP-2000; 2000US-0236357P.
29-SEP-2000; 2000US-0236363FP.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-CCT-2000; 2000US-0236369P.
02-CCT-2000; 2000US-0237039P.
02-CCT-2000; 2000US-0237039P.
02-CCT-2000; 2000US-0237039P.
03-CCT-2000; 2000US-0237039P.
03-CCT-2000; 2000US-0237039P.
03-CCT-2000; 2000US-023993FP.
03-CCT-2000; 2000US-023493FP.
03-CCT-2000; 2000US-0241868P.
03-CCT-2000; 2000US-0246474P.
03-CCT-2000; 2000US-0246474P.
03-CCT-2000; 2000US-0246474P.
03-CCT-2000; 2000US-0246673P.
03-CCT-2000; 2000US-024673P.
03-CCT-2000; 2000US-024673P.
03-CCT-2000; 2000US-024673P.
03-CCT-2000; 2000US-024673P.
03-CCT-2000; 2000US-024673P.
03-CCT-2000; 2000US-024673P.
03-CCT-2000
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2000US-0250391P.
2000US-0251030P.
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2000US-0249245P.
2000US-0249264P.
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2000US-0249299P.
2000US-0249300P.
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05-DEC-2000; 2
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Barash SC, Ruben SM;

Rosen CA,

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (EILSA) Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac carest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac carest, cerebrovascular disorders e.g. cardiac corest, careforous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, bacteria, viruses and fungi and ocular disorders e.g. corneal infection, can also be used to aid wound healing and epithelial cell proliferation, cor regenerate tissues not chemotaxis. The polypeptides can also be used can also be used to content, lipid, protein, carbohydrate, vitamins, cor expensitities, fat content, lipid, protein, carbohydrate, vitamins, mineralls, cofactors and other nutritional components. The present capabilities and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WTFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
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                                                                                      New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
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                                                                                                                                                                                  Claim 11; SEQ ID NO 809; 980pp; English
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                                             N-PSDB; AAS25843
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2000US-025267P
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2000US-0226868P.
2000US-0228924P.
2000US-0229287P.
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2000US-0229513P
2000US-0231413P
2000US-023423P
2000US-023497P
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2000US-0236327P
2000US-0236367P
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2000US-0236368P
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2000US-0236802P.
2000US-0237037P.
2000US-0237038P.
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2000US-0218290P.
2000US-0220963P.
2000US-0220964P.
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2000US-0239935P.
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2000US-0241809P.
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26-JUL-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
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05-SEP-2000; 2
08-SEP-2000; 2
21-SEP-2000; 2
25-SEP-2000; 2
27-SEP-2000; 2
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29-SEP-2000; 2
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29-SEP-2000; 2
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01-SEP-2000;
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ROSEN C A. RUBEN S M. BARASH S C. (ROSE/) R (RUBE/) R (BARA/) B Barash SC; Rosen CA, Ruben SM,

WPI; 2003-147444/14. N-PSDB; ABX73184. New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.

Claim 11; SEQ ID NO 809; 402pp; English.

The invention relates to human novel polypeptides and their associated polymuclectides. The polypeptides and polymuclectides are useful in gene therapy for treating, inhibiting or preventing neural disorders; immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g.

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nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, agstrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatcry diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scnmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panear IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
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Pred. No. 0.014;
                                                                                                                                                                                                                                                                                        6; Mismatches
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12-SEP-2002; 2002US-0410260P.
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Best Local Similarity 34.8%;
Matches 23; Conservative
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N-PSDB; ACN42006.
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used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, and the disorders autoimmune/inflammatory disorders, developmental disorders, endocrine disorders, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Money EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
  diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosting a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
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(7)
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12-SEP-2002; 2002US-0410260P.
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                                                                                                                                                                                                                                                                                                                                                 23; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                        Sequence 572 AA;
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conclusions also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence at for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panasar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnostic a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               DB 8; Length 612;
                                                                                                                                                                                                                                                                                                                                                                                         Match 25.3%; Score 85; DB 8; Length 612 Local Similarity 34.8%; Pred. No. 0.023; les 23; Conservative 6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human diagnostic and therapeutic pprotein SEQ ID NO:3601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM83352 standard; protein; 612 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2003; 2003WO-US028227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-329368/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 QTGDVI 103
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                                                                                                                                                                                                                                                                                                                                                       Sequence 612 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                          셤
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                             The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A purintelectide of the invention may have a use in gene therappy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine utoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp confections caused by virus, bacteria, fungi or parasite. The dithp collections and also be used in genetic mapping, in identifying individuals committe biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline incention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from NIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                             1 WIFGRNPACDYHLGNISRLSNKHFQIL --XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                              25.3%; Score 85; DB 8; Length 612; 34.8%; Pred. No. 0.023; ive 6; Mismatches 35; Indels
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Otsuki T;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein sequence SEQ ID NO:12128
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB93182 standard; protein; 623 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
            Claim 27; Page; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
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09-JUN-2000; 2000JP-00241899
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hes 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                           SQGDEI 64
                                                                                                                                                                                                                                       Sequence 612 AA;
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                           59
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

[a] an oligo-dr primer and an oligonuclectide comprisentary to the
complementary strand of a polymucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polymucleotide which comprises one of the 5602
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence, where the
coligonucleotide comprises at least 15 nucleotides and the combination of
polymucleotide comprises at least 15 nucleotides and the combination of
coligonucleotide which comprises a selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
gene therapy. The primer sets can be used in antisense therapy and in
gene therapy. The primer sets can be used in antisense therapy and in
gene therapy. The primers are useful for synthesising polynucleotides,
che full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length without any specialised methods. AAH33133 to AAH3383 and
AAH3833 to AAH3832 represent human anno acid sequences; and AAH3829 to AAH3332 represent
coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
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antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 WIGRRRGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDISTSGTVINKLKVVKKQTCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WIFGRNPACDYHLGNISRLSNKHFQIL - - XXXXXXLLNDISTNGTWLNGOKVEKNSNQLL
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Claim 8; SEQ ID NO 12128; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asundi V, Zhang J,
T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 85; DB 4;
Pred. No. 0.023;
6; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human protein SEQ ID NO: 501.
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Yang Y, Wehrman T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention
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oligo-dT primer and an oligonucleotide complementary to

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                                                             The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                58
                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
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                                                                                                                                                                                                                                                                      Gaps
An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.
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                                                                                                                                                                                                                                             DB 5; Length 623;
                                                                                                                                                                                                                                          25.3%; Score 85; DB 5; Length 623
34.8%; Pred. No. 0.023;
ive 6; Mismatches 35; Indels
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, Otsuki 1
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A, Nagai K,
                                       Example 2; SEQ ID NO 501; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:12100.
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T, Wakamatsu
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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les 23, Conservative
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                                                                                                                                                                                                                 Sequence 623 AA;
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                                                                                                                                                                                                                                           Query Match
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complementary strand of a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprises an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end comprises and oligonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence and an oligonucleotide comprises at least 15 nucleotides and the combination of specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in catection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13631 represent human amino acid sequences; and AAH13629 to AAH13632 represent considers allow obtaining of the considering of the considering the considering of the considering the considering the considering the considering and cold sequences; and and AAH13629 to AAH13632 represent considering the used in the exemplification of the considering the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a FHAR1 polypeptide, which is a member of the RING finger protein family. FHAR1 is useful in the treatment of cancer, and as a vaccine for inducing an immunological response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a human ring finger protein designated FHAR1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 85; DB 4; Length 652; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHAR1; RING finger protein; cancer; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB83843 standard; protein; 664 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 19; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chaturvedi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-2000; 2000WO-US033094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.8'
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 SQGDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200142430-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 20
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mammal. FHARI polynucleotides may also be used as a diagnostic reagent through detection of mutations in the associated gene, and for chromosome localization studies, end tissue expression studies. FHARI antibodies are useful to isolate and to identify clones expressing the polypeptides, or to purify the polypeptides by affinity chromatography and to treat cencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of human mitotic checkpoint protein Chfr, having a forkhead associated domain (FHA) and a ring finger domain. The protein is required for regulation of the transition of cells from prophase to metaphase during mitosis. It has ubiquitin-protein ligase activity. The Chfr checkpoint was evident in primary human cells, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                Checkpoint with forkhead associated domain and ring finger; Chfr; human; mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening; ubiquitin-protein ligase.
                                                                                                                                                                          28
                                                                                                                                                                                       Novel nucleic acid sequence of mitotic checkpoint gene encoding a checkpoint with forkhead-associated domain and ring finger protein, for diagnosing tumorigenic cells and in screening for anticancer drugs.
                                                                                                                                                                       1 WTFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                            Gaps
                                                                                                                                             2;
                                                                                                               Score 85; DB 4; Length 664;
Pred. No. 0.025;
6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Human Chfr (checkpoint with FHA and ring finger) protein.
                                                                                                                                          35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31. .103
/label= Forkhead-associated domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Ring_finger-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Met in U2OS cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476. .641
/note= "cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WIST-) WISTAR INST ANATOMY & BIOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8(a); Fig 4A-C; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   AAB20219 standard; protein; 664 AA
                                                                                                               ch 25.3%;
1 Similarity 34.8%;
23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                             98 QTGDVI 103
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N-PSDB; AAF30352.
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                                                                                                                                                                                                                                  SQGDEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200109150-A2
                                                                                     Sequence 664
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                                                                                                               Query Match
Best Local
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                                                                                                                                            Matches
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c inactivated in 4 of 8 human cancer cell lines. In UZOS cells, a mutation was identified that caused a Val to Met amino acid substitution in the highly conserved C-terminal Cys-rich region of the Chfr protein. In the absence of the Chfr checkpoint, calls subjected to mitotic stress condensed thair chromosomes despite failing to separate their chromosomes Chfr may monitor centrosome separation. Inactivation of the chromosomes. Chfr may monitor centrosome separation. Inactivation of the chromosomes. Chfr may monitor centrosome separation. Inactivation of the chromosomes. Chfr may monitor centrosome separation. Inactivation of the chromosomes. Chfr may monitor centrosome separation. Inactivation of the comprising the present sequence, or sequences comprising at least amino acids 31-103, 303-346 and/or 476-641 of this sequence, are claimed. Claimed methods of determining the tumourigenic potential of a cell comprise examining the cull for the presence of Chfr expression or for the presence of Chfr expression indicating prediaposition to tumourigenesis upon exposure to mitotic stress). A diagnostic kit for detecting the cumourigenic potential of cell cells comprises may comprise a ligand that binds to Chfr, such as an antibody or its fragment. Inhibitors of Chfr are identified by monitoring their effect on Chfr expression, and are used to retard the growth of cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H1;
therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell cycle regulatory factor-encoding gene for production recombinant proteins with kinase activity, used to develop drugs to treat cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 WIIGERRGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDTSTSGTVINKLKVVKKQTCPL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the human cell cycle regulatory factor das1. The Cds1 nucleotide sequence can be used in gene therapy. Cds1 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISINGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, cell cycle regulatory factor, Cd81; hCd81; cdc25; histone phosphorylation; cancer; proliferative disease; cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 85; DB 4; Length 664
Pred. No. 0.025;
6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cell cycle regulatory factor Cds1 SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 35-39; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY67968 standard; protein; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                25.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 34.8 Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTGDVI 103
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24.3%; Score 81.5; DB 4; Length 288; 38.5%; Pred. No. 0.027; ive 11; Mismatches 24; Indels

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4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen, immunogen, vaccine, tuberculosis, non specific adjuvant, skin testing, M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen TbRa10.
                                                                                                                                                                                                                                                                                                  AAW32352 standard; protein; 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed SG, Skeiky YAW, Dillon DC,
Vedvick TH, Twardzik DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                      Query Match 24.3%
Best Local Similarity 38.5%
Matches 25; Conservative
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22-MAR-1996;
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                                                                                                                                                                                                                                                                RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These ret useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and corpused in procession vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                              be used to detect inhibitors of cell cycle regulatory factors which can be applied in the development of drugs for treating cancers and proliferative diseases. Cds1 is strongly expressed in the testis as well as other tissues. Cds1 can efficiently phosphorylate cdc25 and histone H1
                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                          1 WIFGRNPACDY-----HLGNISRLSNKHFQIL----XXXXXXLLNDISTNGTWLNG
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; SEQ ID NO 3552; 246pp + Sequence Listing; English
                                                                                                                                25.0%; Score 84; DB 3; Length 543; 29.1%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ochiai K,
                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum protein fragment SEQ ID NO: 3552
                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  ż
                                                                                                                                                                                                                                                                                                        ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                                                                                                            AAG89798 standard; protein; 288
                                                                                                                                                                                                                                                                                 OKVEKNSNQLLSQGDEITV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                      23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mizoguchi F
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-376931/40.
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH65017.
                                                                                             Sequence 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG89798;
                                                                                                                                Query Match
                                                                                                                                                     Local
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                         AAG89798
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                                                                                                                                                                                                         immunogenic part of a soluble mycobacterium tuberculosis antigm (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TARA10. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RLSNXHFQILXXXXXXLLNDI-STNGTWLNGQKVEXNS 54
       tuberculosis antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                               A new immunogenic polypeptide has been developed comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 23
immunogenic polypeptide(s) from soluble M. tu ul for diagnosis of M. tuberculosis infection
                                                                                                                Example 3; Page 100-101; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GRNPACDYHLGNIS --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.7
Best Local Similarity 28.8
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             also used for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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Sequence 288 AA;

Campos-Neto A, Houghton R;

95US-00523435. 95US-00532136. 96US-00620280. 96US-00658800.

96WO-US014675

(first entry)

TbRa10.

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Tuberculosis; infection; diagnosis; antigen;
                                                                                        Mycobacterium tuberculosis antigen TbRa10.
                                                                                                                                tuberculosis; strain H37Ra
                    AAW64292 standard; protein; 148 AA.
                                                                                                                                                                                           97WO-US018214.
                                                                                                                                                                                                             96US-00729622.
97US-00818111.
                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                         N-PSDB; AAV44340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 148 AA;
                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Sim-
                                                                                                                                                   WO9816645-A2
                                                                                                                                                                                          07-OCT-1997;
                                                                                                                                                                                                             11-OCT-1996;
13-MAR-1997;
                                                         17-OCT-2003
09-NOV-1998
                                                                                                                                                                       23-APR-1998
                                        AAW64292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81655
          AAW64292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TDRa10. The immunogenic protein, and fusion proteins containing one or more of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 GRHPDSDIFLDDVTVSRRHAEFRLENNEFNVV------DVGSLNGTYVNREPVD--- 113
 GRHPDSDIFLDDVTVSRRHAEFRLENNEFNVV------DVGSLNGTYVNREPVD--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic polypeptide(s). from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                     Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%; Score 79.5; DB 2; Length 148;
28.8%; Pred. No. 0.022;
.ive 16; Mismatches 15; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new immunogenic polypeptide has been developed comprising an
                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                   Houghton
                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A,
                                                                                                                                                   Mycobacterium tuberculosis antigen TbRa10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 94; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
DR;
                                                                                       AAW32420 standard; protein; 148
                                                                                                                                                                                                                                                                                  95US-00523436.
95US-00533634.
96US-00620874.
96US-00659683.
                                                                                                                                                                                                                                                                96WO-US014674
                                                                                                                                                                                                     Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAVLANGDEVQIG 126
                              : :|: |||: :|
114 SAVLANGDEVQIG 126
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                  55 NOLLSOGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 28.8
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 NOLLSQGDEITVG
                                                                                                                                                                                                                                                                                                                                                                            Twardzik
                                                                                                                                                                                                                                                                                                                                                                   Skeiky YA,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-192903/17.
                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT91465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 148 AA;
                                                                                                                                                                                                                                                               30-AUG-1996;
                                                                                                                                                                                                                        409709428-A2
                                                                                                                                                                                                                                                                                   01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                            Vedvick TH,
                                                                                                                                                                                                                                                                                                        22-MAR-1996;
                                                                                                                                                                                                                                                                                                                05-JUN-1996;
                                                                                                                                                                                                                                             13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis
                                                                                                           AAW32420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
                                                                                                                                                                                                                                                                                                                                                                   Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                    RESULT 25
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This polypeptide comprises Mycobacterium tuberculosis soluble antigen This polypeptide comprises Mycobacterium tuberculosis strain H37Rs expression library with rabbit anti-sera raised against M. tuberculosis supernatant. No significant homology was found between TDRa1 and Genebank database sequences. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAM64391-W6439) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis infection vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using the above detecting M. tuberculosis of infection in a patient using the above diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                          New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                          Campos-Neto A, Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                      Dillon DC, Ca
DR, Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 99; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW81655 standard; protein; 148 AA.
                                                                  Reed SG, Skeiky YAW, Dill
Vedvick TS, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAVLANGDEVQIG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                    WPI; 1998-251292/22.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Houghton R;

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66 GRHPDSDIFLDDVTVSRRHAEFRLENVV------DVGSLNGTYVNREPVD--- 113
                                                                                                                                                                                                                                                                                                                                      This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS
                                                                                                                                                                                                                                                                   New polypeptide comprising antigenic portions of M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 21
                                                                                                                                                          Campos-Neto A, Ho
J, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Ho
Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis antigen TbRa10 amino acid sequence.
                                                                                                                                                                             Lodes MJ,
                                                                                                                                                                                                                                                                                                    Example 3; Page 136; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY39094 standard; protein; 148 AA.
                                                                                                                                                          Dillon DC,
                                                                    98US-00024753
98US-00072596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00025197
98US-00072967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|:|||::|
114 SAVLANGDEVQIG 126
                                                                                                                                                                             Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 28.8 les 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 NOLLSOGDEITVG
                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                              WPI; 1999-527416/44.
N-PSDB; AAZ19038.
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                                                                                                                         (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 148 AA;
                                                                    18-FEB-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1998;
                                    17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1999
                                                                                                                                                                             Vedvick TS,
 26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY39094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                     Tuberculosis, immunogenic; soluble, antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                             Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. tuberculosis recombinant antigen protein TbRa10.
                                                                                                                                                                                                                                                                                                                                                                                             Campos-Neto A,
                                                                  M. tuberculosis immunogenic polypeptide TbRa10
                                                                                                                                                                                                                                                                                                                                                                                         Dillon DC, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 96; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY38957 standard; protein; 148 AA.
                                                                                                                                                                                                                                                                                                   96US-00730510.
97US-00818112.
                                                                                                                                                                                                                                                                 97WO-US018293,
                                                                                                                                                        Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|:||||::|
SAVLANGDEVOIG 126
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis of tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
3, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV64448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 148 AA;
                                                                                                                                                                                                                                                              07-OCT-1997;
                                                                                                                                                                                           WO9816646-A2
                                                                                                                                                                                                                                                                                                   11-OCT-1996;
                                                                                                                                                                                                                                                                                                                     13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9942118-A2
                                 27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                         Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1999
                                                                                                                                                                                                                              23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY38957;
AAW81655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
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Matches
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The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A; CFP19; CFP19; CFP19; CFP10A; CFP10A; CFP10B; CFP19; CFP19; CFP10B; CFP10
                                                                                                                                                                                                                                                                                                                              Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic fragment of Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                           23.7%; Score 79.5; DB 2;
28.8%; Pred. No. 0.024;
iive 16; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of antigen CFP17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 59; 265pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY21903 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97DK-00001277.
98US-0070488P.
98WO-DK000132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-DK000438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|:|||::|
127 SAVLANGDEVOIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                           Local Similarity 28.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 NQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CFP25A; CFP30B; CFP7B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersen P, Skjot R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-347282/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX81003
                                                                                                                                                                                                                                                                     Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9924577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-1998;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY21903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥8888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                               The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ1929 to AAZ192460 and AAX19083 to AAX19225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen;
                                                      New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rasmussen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosenkrands I, Weldingh K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis antigen CFP17.
                                                                                                                                               Example 3; Page 96-97; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1, Page 127-128; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW72886 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0044624P.
97DK-00001277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-DK000132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97DK-00000376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0070488P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAVLANGDEVQIG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 NQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nielsen R,
Florio W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-542705/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV63917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersen P,
Oettinger T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9844119-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1997;
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10-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW72886;
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are useful as pharmaccuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or response in a mammal, use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for the induction of a strong immune response in a mammal, use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF5, MPT59-ESAT6, ESAT6-MPT59, CFP10A, CFP10A, CFP13, CFP25A, CFP30B, CFP7B or a T-cell epitope of for the preparation of an immunological composition; and for the preparation of a subunit vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of the Mycobacterium tuberculosis (Mtb) strain H37Rv gene Rv1827 product, designated CP17. This is one of 31 immunodominant secreted or cytosolic Mtb proteins of strain H37Rv (see AAM50729-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and liquid chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity to mycobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BCG and in whom
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRHPDSDIFLDDVTVSRRHAEFRLENVV------DVGSLNGTYVNREPVD--- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 life in a subject who has been vaccinated in childhood with Bacillus
Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine for boosting immunity to mycobacteria when administered in mid-
The polypeptides and nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                             GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGOKVEKNS
                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                         23.7%; Score 79.5; DB 2; Length 162; 28.8%; Pred. No. 0.024; tive 16; Mismatches 15; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis immunodominant Mtb protein CP17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogen; mycobacteria; immunisation; vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COLS ) UNIV COLORADO STATE RES FOUND.
encodes the above polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM50735 standard; protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 17; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2001; 2001WO-US021717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAVLANGDEVQIG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOLLSQGDEITVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Belisle JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-164602/21.
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                    Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200204018-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mtb; CP17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
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                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM5073
8888888888888888888888888888888888
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                                                                                                                                                            47
                                                                                                                                               4 GRNPACDYHLGNIS------RLSNRHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WIFGRNPACDY------HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
                                                                                                                      21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is the protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New gene encoding a protein for inhibiting human Chk2 phosphoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Indels 14;
                                                                                         23.7%; Score 79.5; DB 5; Length 162; 28.8%; Pred. No. 0.024; ive 16; Mismatches 15; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                    Human; Chk2 phosphoenzyme inhibitor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 13-16; 36pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                           Human Chk2 phosphoenzyme inhibitor.
                                                                                                                                                                                                                                                                                            AAM48994 standard; protein; 514 AA.
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128 SAVLANGDEVQIG 140
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                                                                                         Query Match
Best Local Similarity 28.8
Matches 21; Conservative
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                                                                                                                                                                                                   55 NOLLSQGDEITVG
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Best Local Similarity
'...hes 22; Conserve
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                                                                  Sequence 162 AA;
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                                                                                                                                                                                                                                                                                                                                                 08-JUL-2002
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RESULT

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The present invention describes a method for detecting a cancer cell in a subject, which comprises determining the level of nucleic acid that is subject, which comprises determining the level of nucleic acid or polypeptide is indicative of cancer in the subject. Also product in a sample of the subject, where an elevated level of the concernence of a cancer in a subject comprising a cancer or predicting recurrence of a cancer in a subject comprising a cancer or predicting recurrence of a cancer in a subject comprising a cancer or predicting recurrence of a cancer in a subject comprising a cancer cell; (3) an isolated or protein encoded by a nucleic acid as described above; (2) the isolated or complex; (5) a kit for detecting cancer cell; (3) an isolated or recombinant protein complex; (4) an antibody that binds to the protein complex; (5) a kit for detecting or producing a protein complex; (5) a kit for detecting or producing a protein complex; (5) a kit for detecting or producing a protein complex; (6) a kit for detecting or protein of an EDD polypeptide or a portion of an EDD polypeptide or a portion of an EDD polypeptide or the protein complex; (7) a method for determining a protein protein of the cancing or the portion of an EDD polypeptide; (6) methods for isolating the protein complex; (7) a method for determining a predisposition for disease, or disease state; (8) a method for determining a modulator of the activity, commation; (10) a method for determining a modulator of the level of protein complex; (6) a method for treating a condition associated with celevated expression of EDD protein in a cell; (11) an antisense nucleic acid, ribozyme, PNA, interfering RNA or siRNA, and (12) a pharmaceutical composition comprising the antisense nucleic acid, ribozyme, PNA, interfering RNA or siRNA, EDD has cytostatic activity, and can be used in gene therapy. The methods and modulator are useful for treating a condition associated with EDD over expression such as cancer.
                                                                                                                                                                                                       detection; cancer; 8q22.3; chromosome 8; human; EDD; tumour suppressor; cell cycle modulator; DNA repair; DNA damage; nuclear targeting protein; progesterone receptor; cytostatic; gene therapy; squamous cell carcinoma; hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma; hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma; gastrointestinal cancer; renal cell cancer; bladder cancer; prostate cancer; non-squamous lack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a cancer cell in a subject sample, also related to cancer treatments, comprises determining the level of nucleic acid that is linked to map position 8q22.3 of the human genome or its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clancy J, Henshall S;
                                                                                                                                                             Human Chk2 transcript variant 2 protein SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 29; SEQ ID NO 21; 331pp; English.
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P;
                     ADL32563 standard; protein; 514 AA
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                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                              variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watts C, Saunders D,
Sutherland R, O'brien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADL32562
                                                                                                                                                                                                                                                                                                                                                                            Chk2 transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004022750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                               03-JUN-2004
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4DL32563
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breast cancer, melanoma, hepatocellular carcinoma, ovarian cancer, breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous breast cancer, gastroincestain cancer (eg. gastric, colon, or pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous carcinoma, glioblastoma and medullablastoma. The components and composition are useful for reducing the expression of EDD in a cell to inhibit cellular proliferation. The present sequence represents human chk2 transcript variant 2 protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a number of peptides which disrupt the G2 cell cycle checkpoint when administered to a cell. They act by inhibiting Chk2 (the sequence of which is shown here) and Chk1 kinases, and may be derived from Cdc25C. The peptides are useful in the treatment of cell proliferation diseases, such as cancer, as the inhibition of the Chks allows DNA damage and induces apoptosis
                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Cdc25C; Chk1; Chk2; G2 checkpoint; cell cycle regulation; cancer; cell proliferation; apoptosis.
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                                                                                                                                                                                                                                                                1 WIFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated or recombinant polypeptide of 7-11 amino acids, useful for treating cell proliferative disorders, e.g. to stop the growth of, or kill cancer cells, by disrupting the G2 cell cycle arrest checkpoint.
                                                                                                                                                                                                                                14;
                                                                                                                                                                                                  Length 514;
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                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                32;
                                                                                                                                                                                                 22.9%; Score 77; DB 8; 27.8%; Pred. No. 0.23;
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                                                                                                                                                                                                                               11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Chk2 kinase protein sequence.
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                                                                                                                                                                                                                                                                                                                                                              173 ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG68375 standard; protein; 542
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                                                                                                                                                                                                                                Conservative
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nes 22, Conserv
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les 22; Conserv
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                                                                                                                                                                    Sequence 514 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200121771-A2
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30-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG68375;
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Matches
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Gaps

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32;

Conservative

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22-OCT-1997;
                                                                                                                                 Homo sapiens
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                                                          02-AUG-1999
                                                                                                                                                                        29-APR-1999.
                                       AAY05765;
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RESULT 37
           AAY05765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a novel human checkpoint kinase, termed hCDS1, that acts in coordination with Cdc25 in the DNA damage checkpoint. The sequence is predicted from a CDNA (see AAXS8793) isolated from a SK-N-MC neuroblastoma cDNA library. The predicted protein is 28% identical to the cdc1 protein of S. pombe. A 2.2 kb transcript is expressed in testis and in 8 human cancer samples examined. hCDS1, its inhibitors and activators, are useful for treating cancer or proliferative disease (claimed). Inhibitors and activators of the kinase activity can also be used in anti-cancer therapy, particularly by increasing susceptibility of cancer cells to chemotherapy and/or radiotherapy (claimed). hCDS1 is useful for modifying DNA damage checkpoint activity of a cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 W-FGRDKSCEYCFDEPLLKRTDKYRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNT 171
                                                                                                                                                                                                                                                                                                                                                                                                                     New human kinase used for treatment of cancer and proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WIFGRNPACDY------HLGNISRLSNKHFQIL----XXXXXXLLNDISTNGTWLNG 47
         WIFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                    Checkpoint kinase; hCDS1; human; DNA damage; proliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.9%; Score 77; DB 2; Length 543; 27.8%; Pred. No. 0.24; ive 11; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                    Blasina A;
                                                                                                                                                                                                                                                                                                                                                                    Mcgowan C,
                                                                                                                      AAY06204 standard; protein; 543 AA.
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                                                                  172 ELVGKGKRRPLNNNSELAL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 OKVEKNSNOLLSOGDEITV 66
                                                99
                                                                                                                                                                                Human checkpoint kinase hCDS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Fig 2; 39pp; English
                                                                                                                                                                                                                                                                                               98WO-EP006981.
                                                                                                                                                                                                                                                                                                                  97GB-00022320.
                                                OKVEKNSNQLLSQGDEITV
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Best Local Similarity 27.00,
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Luyten WHML, Parker AE,
                                                                                                                                                                                                                                                                                                                                     (SCRI ) SCRIPPS RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX58793
                                                                                                                                                                                                               cancer; therapy
                                                                                                                                                                                                                                                                                              21-OCT-1998;
                                                                                                                                                                                                                                                       WO9925843-A2
                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                  22-OCT-1997;
                                                                                                                                                             16-AUG-1999
                                                                                                                                                                                                                                                                          27-MAY-1999.
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                                                                                                  RESULT 36
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The present sequence represents hCDS1, a novel human cell cycle checkpoint kinase that acts in coordination with Cdc25 at the DNA damage checkpoint, rather than the replication checkpoint as found in yeast. The hCDS1 sequence was predicted from hCDS1 cDNA (see AAX25464) that was chearing a sequence was predicted from hCDS1 cDNA (see AAX25464) that was cobtained from a human SK-N-MC neuroblastoma cDNA library. It shows 28% contity with cds1 protein of S. pombe, 28% identity to RAD53 and 27% identity to the DWN kinase of S. cerevisiae. Northern blot analysis cidentified a single transcript of about 2.2 kb expressed in testis and in 8 human cancer samples examined. The characterisation of hCDS1 and the clucidation of flar role in the DNA damage checkpoint allows for the clucidation of pharmaceuticals and therapeutic methods for acting as an adjunct to chemotherapy of cancer. Thus, pharmaceutical formulations can this object and the angalant continuous definition and the protein, or other therapeutics identified in caseays of the invention, can be administered in conjunction with any suitable chemotherapy agent to act as an adjunct to the main action of the chemotherapy agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                                                         Ccell cycle checkpoint kinase; human; hCDS1; cell proliferation; cancer; therapy; chemotherapy; adjunct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human cell cycle checkpoint kinase hCDS1, useful for treating cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WIFGRNPACDY-----HIGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation diseases, e.g. cancer.
                                                                                                                                                                                           Novel human checkpoint kinase hCDS1
AAY05765 standard; protein; 543 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 33-34; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luyten WHML, Parker AE;
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Best Local Similarity
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AAM48996
ID AAM48
XX
AC AAM48
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Gaps

14;

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The invention relates to an antisense compound targeted to a nucleic acid molecule encoding human checkpoint kinase 2 (CHK2). The antisense compound specifically hybridises with and inhibits the expression of human CHK2. The antisense compounds are useful as research reagents and diagnostics, in distinguishing between functions of various members of a closical pathway, and in the treatment of a disease or disorder, which can be treated by modulating the expression of CHK2. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         114 W-FGRDKSCEYCFDEPLLKRTDKYRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNT 172
                                                                                                                               The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense oligonucleotides targeted to a nucleic acid encoding checkpoint kinase 2 (CHK2), useful for treating a disease or condition associated with CHK2, or in distinguishing functions of members of a
                                                                                                                                                                                                                                                                                                                                                                               1 WIFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
                  encoding a protein for inhibiting human Chk2 phosphoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               checkpoint kinase 2; CHK2; enzyme; antisense therapy
                                                                                                                                                                                                                                                                                         Length 543;
                                                                                                                                                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                         ; Score 77; DB 5;
; Pred. No. 0.24;
11; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human checkpoint kinase 2 (CHK2) polypeptide.
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                                                                                        Disclosure; Page 20-23; 36pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG30701 standard; protein; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OKVEKNSNQLLSQGDEITV 66
                                                                                                                                                                                                                                                                                         22.9%;
ilarity 27.8%;
Conservative 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sarthy A, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-575367/61.
N-PSDB; ABK88909.
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                 Sequence 543 AA;
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                         New gene activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG30701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.
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                                                              Human Chk2 phosphoenzyme inhibitor related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Chk2 phosphoenzyme inhibitor related protein #1.
                                                                                                             Human; Chk2 phosphoenzyme inhibitor; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Chk2 phosphoenzyme inhibitor; cytostatic
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                       (first entry)
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N-PSDB; AAL44750.
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les 22; Conserv
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3;
Query Match 22.9%; Score 77; DB 5; Length 543; Best Local Similarity 27.8%; Pred. No. 0.24; Matches 22; Conservative 11; Mismatches 32; Indels 14; Gaps
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HLGNISRLSNKHFQIL	<u>-</u>	114 W-FGRDKSCEYCFDEPLLKRTDKYRTYSKKHFRIFREVGPKNSYI
1 WIFGRNPACDY	- -	4 W-FGRDKSCEYCFDEPLL
۸۵	,	Db 11,

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⁴⁸ QKVEKNSNQLLSQGDEITV 66 : | | : | | : 173 ELVGKGKRRPLNNNSEIAL 191

Search completed: February 24, 2005, 15:19:39 Job time : 143.537 secs

Sequence Sequence Sequence Seguence

Sequence 16276, A Sequence 45, Appl Sequence 22, Appl Sequence 21, Appl Sequence 21, Appl Sequence 41, Appl Sequence 12792, A Sequence 755, Appl Sequence 755, Appl Sequence 22693, A Sequence 48, Appl Sequence 11336,
us-09-936-956-19.rai

Run on:

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1 WIFGRNPACDYHLGNISRLSNKHFQIL--LGNLLLNDISTNGTWLNGQKVERNSNQLLSQ
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                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 46, Application US/09300008B
; Batent No. 6458534
; GENERAL INFORMATION:
; APPLICANT: CONCENTON et al.
; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE
; TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEI
; FILE REFERENCE: 9924-0003-228
; CURRENT APPLICATION NUMBER: US/09/300,008B
; CURRENT FILING DATE: 1999-04-27
; PRIOR PILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FREESEQ for Windows Version 3.0
; LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 93.8%; Score 315; DB 4; Length 65; I Similarity 91.0%; Pred. No. 6.6e-36; 61; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
STRET: 1420 Pifth Ave., Suite 2800
CITY: Seattle
STATE: Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 17, Application US/08198446B
; Patent No. 5674996
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Plon, Sharon B.
; APPLICANT: Plon, Sharon B.
; APPLICANT: Groudine, Mark T.
; TILE OF INVENTION: Cell Cycle Checkpoint Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
                         US-09-849-617-2
US-09-902-540-1521
US-09-902-540-1521
US-09-300-008B-45
US-09-919-172-98
US-09-916-594-22
US-09-916-919-019-21
US-09-300-008B-41
US-09-300-008B-41
US-09-902-540-12792
US-09-902-540-12792
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US-09-252-991A-22693
US-09-300-008B-48
US-09-902-540-11336
                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-300-008B-46
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Best Local Similarity
               RESULT 1
US-09-300-008B-46
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Sequence 18515, A
Sequence 18515, A
Sequence 1334, A
Sequence 10544, A
Sequence 10597, A
Sequence 14372, A
Sequence 14372, A
Sequence 14372, A
Sequence 17202, A
Sequence 18516, A
Sequence 18516, A
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                                                                                                     February 24, 2005, 15:14:52 ; Search time 33.7724 Seconds
(without alignments)
148.094 Million cell updates/sec
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?: /cgn2 6/ptodata1/iaa/5B_COMB.pep:*
. /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
. /cgn2 6/ptodata1/iaa/6B_COMB.pep:*
. /cgn2 6/ptodata1/iaa/BCOMB.pep:*
. /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
. /cgn2 6/ptodata1/iaa/backfiles1.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-198-446B-17
US-08-198-446B-17
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US-08-198-446B-6
US-09-30-008B-4
US-09-302-540-1336
US-09-902-540-1334
US-09-902-540-16334
US-09-902-540-1637
US-09-902-540-10597
US-09-902-540-10597
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US-09-902-540-1056
US-09-902-540-1056
US-09-902-540-1056
US-09-902-540-1056
US-09-902-540-1059
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US-09-949-016-10788
US-09-529-093A-2
US-09-529-154-2
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                                                                                                                                                                                                                                                                         513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2.97.5
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2.97.5
770.7
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770.7
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                                                                                                                                                                                                  Sequence:
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No.

Result

THEIR USE

9 58

Gaps

2;

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FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
ATTORNEY AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR110798
TELECHONE 206-682-8100
TELEPHONE: 206-682-8100
TELEPHONE: 206-682-8100
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 amino acids
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
DESCRIPTION: yeast MEC2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08198446B Patent No. 5674996
                                                                                                                                                                                                                                                                   LENGTH: 776 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                821 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 206-224-0779
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||||
126 QGDEITVG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%; Score 313.5; DB 1; Length 776; 89.7%; Pred. No. 2.2e-34; tive 0; Mismatches 6; Indels 1
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Patent No. 5866338

GENERAL INFORMATION:

APPLICANT: Hartwell, Leland H.

APPLICANT: Plon, Sharon B.

APPLICANT: Plon, Sharon B.

TITLE OF INVENTION: Cell Cycle Checkpoint Genes

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC

STREET: 1420 Fifth Ave., Suite 2800
                                         COMPUTER FELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,446B
FILING DATE: 18-FEB-1994
CLASSIFICATION: 536
ATTONEY/AGENT INFORMATION:
NAME: Sheiness, Diama K.
REGISTRATION NUMBER: 35,356
REPERENCE/DOCKET NUMBER: 35,356
REPERENCE/DOCKET NUMBER: 20,356
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
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ZIP: 98101-2347
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/198,446
FILING DATE: FEBTUARY 18, 1994
APPLICATION NUMBER: PCT/US93/04458
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein

BESCRIPTION: yeast MEC2 protein
US-08-198-446B-17
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 206-224-0//>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
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126 QGDEITVG 133
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Best Local Similarity
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US-08-870-693-17
         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
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66 WTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                    1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                           1; Gaps
     DB 2; Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Weinvell, Leland H.
APPLICANT: Weinvell, Leland H.
APPLICANT: Wordine, Mark T.
APPLICANT: Plon, Sharon E.
APPLICANT: Plon, Sequence: 19
CORRESPONDENCE ADDRESS:
STREET: 1420 Fifth Ave., Suite 2800
COTTY: Seattle
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,446B
FILING DATE: US-08/1994
CLASSIFICATION: 536
ATTONREY/AGENT INFORMATION:
NAME: Sheines, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR17537
TELEPROMUNICATION INFORMATION:
TELEPRAS: 206-224-0779
Query Match 93.3%; Score 313.5; DB 2; Best Local Similarity 89.7%; Pred. No. 2.2e-34; Matches 61; Conservative 0; Mismatches 6;
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1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                                  US-09-248-796A-18515; Sequence 18515, Application US/09248796A; Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Schizosaccharomyces pombe US-09-300-008B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.2%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Candida albicans
US-09-248-796A-18515
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                                                                                                                    126 QGDEITVG 133
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                                                                                60 QGDEITVG 67
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LENGTH: 64
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                                                                                                                                                           66 WTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                                      1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                     Gaps
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                                                              DB 1; Length 821;
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89.7%; Pred. No. 2.3e-34;
iive 0; Mismatches 6; Indels 1
                                                          ch 93.3%; Score 313.5; DB 1; Length 1 Similarity 89.7%; Pred. No. 2.3e-34; 61; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Christensen O'Connor Johnson Kindness PLLC 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: WA

ZIP: 98101-2347

COMPUTER READABLE FORM:
MEDIUM TYPE: FI-DAPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
FILING APPLICATION 536
PRIOR APPLICATION NUMBER: US 08/198,446
FILING DATE: February 18, 1994
APPLICATION NUMBER: PCT/US93/04458
APPLICATION NUMBER: PCT/US93/04458
                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08870693
; Patent No. 5866338
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Plon, Sharon B.
; APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson Kindness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
ATTORNEY,AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REPERENCH/OCKT NUMBER: 35,356
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
DESCRIPTION: yeast MEC2 protein
DESCRIPTION: yeast MEC2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 821 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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|126 QGDEITVG 133
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Best Local Similarity
Matches 61; Conserva
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US-08-198-446B-6
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US-08-870-693-6
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                                                          Query Match
Best Local
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GENERAL INPORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TILL REFERENCE: 107196.132

CURRENT PAPLICATION NUMBER: US /09/248,796A

CURRENT PILING DATE: 1999-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

RIOR FILING DATE: 1998-08-13

RIOR FILING DATE: 1998-08-13

REOR FILING DATE: 1998-08-13
66 WIFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 WYFGRDPNSDLQVASSSKISNKHFQIWLNFNDKSLWIKDTSTNGTHLNNSRLVKGSNYLL 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: CONCANNO et al.
TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE
FILE REFERENCE: 924-0003-228
FILE REFERENCE: 924-003-228
CURRENT APPLICATION NUMBER: US 60/083,269
PRIOR PLING DATE: 1999-04-27
PRIOR PLING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WTFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXXL-LNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
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Pred. No. 3.2e-14;
9; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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41.8%; Score 140.5; DB 4;
Best Local Similarity 46.3%; Pred. No. 6e-12;
Matches 31; Conservative 13; Mismatches 20;
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248 DGDE 251
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US-09-902-540-16334

Patent No. 683447

GENERAL INFORMATION:

APPLICANT: Gldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiggand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 16334
                                                                                                 RESULT 8

US-09-902-540-13360

i Sequence 13360, Application US/09902540

i Patent No. 683347

i GENERAL INFORMATION:

i APPLICANT: Goldman, Barry S.

i APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

i APPLICANT: Misegand, Roger C.

i TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION MUMBER: 60/217,883

PRIOR PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13360

LENGTH: 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 GRSSELDWYLGE-DWYSRKHARISFSDGSITIEDLGSTNGTFVNGEKVKQSR---LKEGD 87
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28.1%; Score 94.5; DB 4; Length 595;
Best Local Similarity 35.4%; Pred. No. 0.00019;
Matches 23; Conservative 17; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.1%; Score 94.5; DB 4; Length 103; Best Local Similarity 36.9%; Pred. No. 2.2e-05; Matches 24; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13360
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58 GDEIRIG 64
61 GDEITVG 67
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EISMG 83
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88 RILIG 92
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Sequence 10597, Application US/09902540
; Sequence 10597, Application US/09902540
; Patent No. 683147
; GRNERAL INFORMATION:
   APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miscand, Myxococcus xanthus Genome Sequences and Uses Thereof;
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
TITLE REPERBNCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT PILING DATE: 2001-07-10
; PRIOR PILING DATE: 2000-07-10
; PRIOR PILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15597
RESULT 10
US-09-902-540-10544

i Sequence 10544, Application US/09902540

i Patent No. 683347

i GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Glodman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Misgand, Roger C.

APPLICANT: Misconceus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 39-1015849) B

CURRENT APLICATION NUMBER: 0/9902,540

CURRENT PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 10544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WIFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-SINGTWLNGQKVEKNSNQLLS 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.8*; Score 93.5; DB 4; Length 311; Best Local Similarity 30.9*; Pred. No. 0.00012; Matches 21; Conservative 15; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Myxococcus xanthus
US-09-902-540-10597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Myxococcus xanthus US-09-902-540-10544
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US-09-252-991A-17202
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US-09-902-540-10166
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Sequence 1372, Application US/09902540
; Patent No. 683347;
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
FRIOR FILING DATE: 2001-07-10
FRIOR FILING DATE: 2000-07-10
WHMBER OF SEQ ID NOS: 16825
SEQ ID NO 14372
LENGTH: 614
                                                                                                                                                                                                                                                                                                                                                                                                   4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.9%; Score 87; DB 4; Length 476; Best Local Similarity 36.9%; Pred. No. 0.0015; Matches 24; Conservative 10; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 25.6%; Score 86; DB 4; Length 614; Similarity 34.8%; Pred. No. 0.0029; 24; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Myxococcus xanthus
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98 KPTDQVYIG 106
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US-09-902-540-14372
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Best Local S
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ORGANISM:
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, Sequence 17202, Application US/09252991A , Patent No. 6551795

US-09-252-991A-17202

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US-09-248-796A-18516;
Sequence 18516, Application US/09248796A;
Sequence 18516, Application US/09248796A;
GREEAL INFORMATION:
APPLICANT: Keith Weinstock et al;
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PELLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17202
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| Patent No. 6833447
| Facinit No. 6833447 |
| GENERAL INFORMATION:
| APPLICANT: Goldman, Barry S. |
| APPLICANT: Blater, Steven C. |
| APPLICANT: Wiegand, Roger C. |
| APPLICANT: Wiegand, Roger C. |
| TILE REFERENCE: 38-10(15849) B. |
| CURRENT APPLICATION NUMBER: US/09/902,540 |
| FILE REPRENCE: 2000-07-10 |
| PRIOR APPLICATION NUMBER: 60/217,883 |
| PRIOR FILING DATE: 2000-07-10 |
| NUMBER OF SEQ ID NOS: 16825 |
| SEQ ID NO 10166 |
| LENGTH: 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.4%; Score 85.5; DB 4; Length 558; 33.3%; Pred. No. 0.003; ive 13; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Myxococcus xanthus
US-09-902-540-10166
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129 P--LRSGDLVKVG 139
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152 QDGETVRLG 160
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                      Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
VENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.7%; Score 79.5; DB 3; Length 148; Best Local Similarity 28.8%; Pred. No. 0.004; Matches 21; Conservative 16; Mismatches 15; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Antonia
APPLICANT: Campos-Netc, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Campos S.
APPLICANT: Campos S.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel R.
                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-1034
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FLING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
MAME: MALL, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELEFANT (206) 622-4900
TELEFANT (206) 622-4900
TELEFANT: (206) 622-631
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/08818111
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : :|: |||: :|
114 SAVLANGDEVQIG 126
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ADDRESSEE: SEED and I
                                                                                                                                                                                          NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                            APPLICANT: Vedvick, APPLICANT: Twardzik, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
USA
                                                                                                                                                                                                                                                                                                            Washington
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US-08-818-112-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6338852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
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CITY: Seattle
STATE: Washingt
COUNTRY: USA
                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
US-08-818-111-65
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                      LOCATION: (4),(9)
CTHER INFORMATION: Identity of amino acid sequences at the above locations are unknous-09-248-796A-18516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16059, Application US/09902540
; Sequence 16059, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Glater, Steven C.
; APPLICANT: Minkle, Gregory J.
; APPLICANT: Wisepand, Roger C.
; APPLICANT: Wisepand, Roger C.
; TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof
; TITLE OF INVENTION: Wyxococcus (S)
; TITLE OF INVENTION NUMBER: 08/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR PRIOR DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WTFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83, DB 4; Length 149;
Pred. No. 0.0013;
8; Mismatches 30; Indels
    FOR DIAGNOSTICS AND THERAPEUTICS
                   FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18516
LENGTH: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-818-112-64

Sequence 64, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 37.5%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16059
                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 33.3
Matches 22; Conservative
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    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDEI 64
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                                                                                                                                                                                                                                                                                                            FEATURE:
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TUBERCULOSIS
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                                                                                                                                                                                                                                                         4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
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                                                                                                                                                ; Score 79.5; DB 3; Length 148;
; Pred. No. 0.004;
16; Mismatches 15; Indels 21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Campos-NetCo. Antonia APPLICANT: Campos-NetCo. Raymond APPLICANT: Houghton, Raymond APPLICANT: Houghton, Raymond APPLICANT: Twardisk, Thomas S. APPLICANT: Twardisk, Daniel R. APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: Codeson, Ronald C. APPLICANT: Compounds and METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REFIRENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky, Yasır A.W.
Dillon, Davin C.
                                                                                                                                                   Query Match 23.7%;
Best Local Similarity 28.8%;
Matches 21; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                          : :|: |||: :|
114 SAVLANGDEVQIG 126
  LENGTH: 148 amino acids
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Best Local Similarity 28.8%
Matches 21, Conservative
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STRANDEDNESS: single
                                                  single
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CITY: Seattle
STATE: Washington
                        TYPE: amino acid;
STRANDEDNESS: si;
TOPOLOGY: linear
US-09-056-556-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/09056556
Fatent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%; Score 79.5; DB 3; Length 148; 28.8%; Pred. No. 0.004; Live 16; Mismatches 15; Indels 2:
                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FLING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERBUELDOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 622-4900
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 148 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : | : | | | : | | | 114 SAVLANGDEVQIG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
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                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
98104-7092
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US-09-056-556-64
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55 NQLLSQGDEITVG 67
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---DVGSLNGTYVNREPVD--- 113
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                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Hondrickson, Ronald C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%; Score 79.5; DB 4; Length 148; 28.8%; Pred. No. 0.004; tive 16; Mismatches 15; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/072,967 FILING DATE: 05-MAY-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | | | | ::
66 GRHPDSDIFLDDVTVSRRHAEFRLENNEFNVV-----
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: smino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        Sequence 64, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-050-739-6

Sequence 6, Application US/09050739
Patent No. 6641814
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :|: |||: :|
114 SAVLANGDEVQIG 126
                          : : | : | | | : |
114 SAVLANGDEVQIG 126
55 NQLLSQGDEITVG 67
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Best Local Similarity 28.8
Matches 21, Conservative
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STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-072-967-64
                                                                                                                                   US-09-072-967-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
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APPLICANT GETTING THE TRANSMESS APPLICANT SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPEC
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GENERAL INFORMATION:
APPLICANT: LUYTEN, Walter H.M.L.
APPLICANT: LUYTEN, Walter H.M.L.
APPLICANT: LUYTEN, Walter H.M.L.
APPLICANT: LUYTEN, Walter H.M.L.
TITLE OF INVENTION: AND WELHOM CHECKPOINT KINASE, hCDS1, COMPOSITIONS
TITLE OF INVENTION: AND METHODS
FILE REPERENCE: JAB 1333 (US)
CURRENT APPLICATION NUMBER: US/09/529,154
CURRENT PILING DATE: 12998-10-21
FRIOR APPLICATION NUMBER: PCT/EP98/06982
FRIOR APPLICATION NUMBER: GB 9722320.0
FRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GSDSACDLVLID-AIVSRRHLEVERTARGLMLRDIGSRNGTFLDGRQVVQ---AYLISGD 105
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849)8 (2009-07-10)
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10583
LENGTH: 459
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.9%; Score 77; DB 4;
Best Local Similarity 27.8%; Pred. No. 0.042;
Matches 22; Conservative 11; Mismatches 3;
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                                                                                                                                                                                              Sequence 2, Application US/09529154
Patent No. 6531312
: | | : |: || : | : 173 ELVGKGKRRPLNNNSEIAL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 EITVG 67
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                                                                                                                                                                 US-09-529-154-2
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                                              US-09-949-016-10788

i Sequence 10788, Application US/09949016

i Patent No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL0001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NO 10788
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| Sequence 2, Application US/09529093A
| Patent No. 6413755
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| Patent No. 6413756
| Patent No. 6413756
| Patent No. 6413756
| Patent Norman Checkpoint Kinase, hCDS1, Compositions and Methods TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods TITLE OF INVENTION NUMBER: US/09/529,093A
| CURRENT PILING DATE: 2000-04-07 | PRIOR PILING DATE: 1998-10-21 | PRIOR FILING DATE: 1998-10-21 | PRIOR FILING DATE: 1997-10-22 | PRIOR PILING DATE: 1997-10-22 | PRIOR PILING DATE: 1997-10-22 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1997-10-22 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1997-10-22 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1998-10-21 | PRIOR PILING DATE: 1
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173 ELVGKGKRRPLNNNSEIAL 191
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 22; Conserva
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ORGANISM: Human
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85 YVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNK 144
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                                                                                                                                                                        APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Wooger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(1549)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15375
LENGTH: 640
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Patent No. 6593110
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: GOZIJIAN
APPLICANT: GUO, ZiJIAN
TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
FILE REFERENCE: CIT1350-1
CURRENT APPLICATION NUMBER: US/09/849,617
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/202,028
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/202,028
NUMBER OF SEQ ID NOS: 14
                                                                                    US-09-902-540-15375
; Sequence 15375, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
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; ORGANISM: Myxococcus xanthus
US-09-902-540-15375
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Matches 20; Conservative
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ORGANISM: Xenopus laevis
US-09-849-617-2
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  106 KVELG 110
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                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Glader, Steven C.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof
FILE REPERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15221
LENGTH: 200
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849) B
CURRENT APPLICANTON NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
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; Patent No. 6458534
; GENERAL INFORMATION:
; APPLICANT: Concannon et al.
; ITILE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.4%; Score 72; DB 4; Length 200; Best Local Similarity 33.3%; Pred. No. 0.061; Matches 22; Conservative 12; Mismatches 26; Indels
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                             Sequence 15221, Application US/09902540
Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Myxococcus xanthus
US-09-902-540-15221
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SEQ ID NO 16276
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Matches 19; Conservative
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JS-09-902-540-15221
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US-09-300-008B-45
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Sequence 20880, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132
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Patent No. 6727066
GENERAL INFORMATION:
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
CURRENT PELICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 66/222,113
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEC ID NOS: 401
SOFTWARE: PERL PROGram
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; OTHER INFORMATION: Incyte ID No. 6727066 2700132CD1
US-09-919-039-21
                                                                                                                                                                                                                                                                      ; NAME/KEY: misc feature
; OTHER INFORMATĪON: Incyte ID No. 6673549 2700132CD1
US-09-976-594-22
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PROL PROGRAM
SEQ ID NO 22
LENGTH: 3256
                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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US-09-248-796A-20980
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Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Purness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
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TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE FILE REFERENCE: 9924-0003-228
CURRENT PAPLICATION NUMBER: US/09/300,008B
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: US 60/083,269
PRIOR PILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 64;
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; OTHER INFORMATION: Incyte ID No. 6673545 2700132CD1
US-09-919-172-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98, Application US/09919172
Patent No. 6673545
GENERAL INFORMATION:
APPLICANT: Faris, Mary
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA.0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT APPLICATION NUMBER: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SEQ ID NO 98
LENGTH: 3256
                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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Matches 20; Conservative
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Best Local Similarity
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US-09-976-594-22
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US-09-919-172-98
                                                                                                                                                                                                                        LENGTH: 64
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Sequence 41, Application US/09300008B

Batent No. 645834

GENERAL INFORMATION:

TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE

TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE

TITLE OF INVENTION: SYNDROME, US/09/300,008B

CURRENT APPLICATION NUMBER: US/09/300,008B

CURRENT APPLICATION NUMBER: US 60/083,269

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 64 0-27

SOFTWARE: PASICEO FOR Windows Version 3.0

LENGTH: 64
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Sequence 42, Application US/09300008B

Batent No. 6458534

GENERAL INFORMATION:

APPLICANT: Concennon et al.

TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE

TITLE OF INVENTION: SYNDROME, US/09/300,008B

CURRENT APPLICATION NUMBER: US/09/300,008B

CURRENT APPLICATION NUMBER: US/09/300,008B

NUMBER OF SEQ ID NOS: 64

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 63
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.5%; Pred. No. 2.9;
Matches 19; Conservative 16; Mismatches 23; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
19.3%; Score 65; DB 4; Length 64;
Best Local Similarity 28.8%; Pred. No. 0.14;
Matches 17; Conservative 10; Mismatches 30; Indels
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
| LENGTH: 883
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 EFDDGDDLT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 Q---GDEIT 65
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-300-008B-42
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Wysococcus xanthus Genome Sequences and Uses Thereof FILE REPERNCE: 3810(15849)B (108740) CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12792
LENGTH: 177
TYPE: PRT
                                                                                                                                                                             3 FGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQGD
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19.0%; Score 64; DB 4; Length 177;
Best Local Similarity 34.5%; Pred. No. 0.66;
Matches 10; Conservative 8; Mismatches 11; Indels
                                                                       Query Match 19.0%; Score 64; DB 4; Length 63; Best Local Similarity 32.8%; Pred. No. 0.19; Matches 21; Conservative 10; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 SMNGTWVNASSLGPDQDRMLNDGDALAFG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12792, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Myxococcus xanthus US-09-902-540-12792
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                  63 EITV 66
                                                                                                                                                                                                                                                                                                                                  59 VİTI 62
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                       US-09-300-008B-42
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February 24, 2005, 15:23:51; Search time 96.9594 Seconds (without alignments) 226.127 Million cell updates/sec
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336
1 WTFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDBITVG
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                   Copyright
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US10_MEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

	Description	Sequence 56, Appl	Sequence 11, Appl	Sequence 16, Appl	Sequence 7635, Ap	Sequence 10, Appl	Sequence 22674, A	Sequence 154547,	Sequence 2299, Ap	Sequence 809, App	Sequence 2, Appli	Sequence 1, Appli	Sequence 3552, Ap	Sequence 156334,
SUMMARIES	QI	US-10-857-622-56	$\boldsymbol{\mathcal{L}}$	US-10-081-119-16		US-09-740-627-10				US-09-764-864-809	US-09-780-525-2	US-09-740-627-1	US-09-738-626-3552	US-10-437-963-156334
	图:	17	σ	14	14	o	15	15	15	σ	σ	O	0	16
	Match Length DB ID	89	522	821	669	460	609	190	474	426	664	543	288	1141
* Ouery	Match	93.3	93.3	93.3	50.0	40.9	27.7	26.5	25.7	25.3	25.3	25.0	24.3	23.8
	Score	313.5	313.5	313.5	168	137.5	93	8	86.5	85	82	84	81.5	80
Result	No.	-	7	m	4	ß	9	7	80	თ	10	11	12	13

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Gaps

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Query Match 93.3%; Score 313.5; DB 17; Length 68; Best Local Similarity 89.7%; Pred. No. 7.7e-34; Matches 61; Conservative 0; Mismatches 6; Indels 1.

Sequence 65, Appl Sequence 64, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 14509, A	Seguence 2, Appli	Sequence 56100, A	Sequence 5092, Ap	Sequence 187236,	Sequence 9, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 1578, Ap	Seguence 2, Appli	Sequence 2, Appli	Sequence 3551, Ap	Sequence 65407, A	Sequence 56757, A	Sequence 163818,	Sequence 233512,	Sequence 13999, A	Sequence 9696, Ap	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 1109, Ap	Sequence 98, Appl		Sequence 174, App	Φ	Sequence 430, App
14 US-10-193-002-65 14 US-10-084-843-64	9 US-09-791-171-6	16 US-10-620-246-6	16 US-10-332-512A-7	14 US-10-156-761-14509	14 US-10-185-182A-2	15 US-10-425-114-56100	9 US-09-738-626-5092	15 US-10-424-599-187236	9 US-09-740-627-9	14 US-10-142-356-6	10 US-09-804-980-6	15 US-10-369-493-1578	9 US-09-849-617-2	15 US-10-618-173-2	9 US-09-738-626-3551	15 US-10-425-114-65407	15 US-10-425-114-56757	16 US-10-437-963-163818	15 US-10-424-599-233512	14 US-10-156-761-13999	14 US-10-156-761-9696	14 US-10-080-170-4	16 US-10-080-170-4	16 US-10-468-356-4	9 US-09-764-864-1109	9 US-09-919-172-98		16 US-10-408-765A-174	16 US-10-701-490-9	15 US-10-389-647-430
148	162	162	162	324	543	1082	143	229	459	545	162	513	517	517	154	617	228	1484	376	843	212	488	488	488	92	3256	3256	3256	3256	397
23.7	23.7	23.7	23.7	23.2	22.9	22.9	22.8	22.8	22.8	22.3	22.2	22.0	21.9	21.9	21.7	20.8	20.5	20.5	20.4	20.4	20.2	20.1	20.1	20.1	19.9	19.9	19.9	19.9	19.9	19.5
79.5	79.5	79.5	79.5	78	77	77	76.5	76.5	76.5	75	74.5	74	73.5	73.5	73	70	69	69	68.5	68.5	68	67.5	67.5	67.5	67	67	67	67	67	65.5
14	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: REBENIS OF THE UNIVERSITY OF COURTERINGS
APPLICANT: VIOLIN, Jonathan
APPLICANT: VIOLIN, Jonathan
APPLICANT: SIEN, Roger
APPLICANT: ZHANG, Jin
APPLICANT: ZHANG, Jin
APPLICANT: ZHANG, Jin
APPLICANT: ZHANG, Jin
APPLICANT: ZHANG, Jin
TITLE OF INVENTION: Emission Ratiometric Indicators of Phosphorylation By C-Kinase
TILE REFERENCE: 39754-0891-CPC1CP2
CURRENT APPLICATION NUMBER: US/10/857,622
CURRENT FILING DATE: 2004-05-24
FRIOR APPLICATION NUMBER: US 09/865,291
FRIOR PILING DATE: 1999-09-13
FRIOR PILING DATE: 1999-09-13
FRIOR PILING DATE: 1996-01-31
FRIOR PILING DATE: 1966-01-31
FRIOR FILING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: phosphoaminoacid binding domain US-10-857-622-56
Sequence 56, Application US/10857622
Publication No. US20050026234A1
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Sequence 7635, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery
TITLE REFERENCE: 10182-005-999
CURRENT PRING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7635
LENGTH: 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 WYFGRDPNSDLQVASSSRISNKHPQIWLNPNDKSLWIKDTSTNGTHLNNSRLVKGSNYLL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 168; DB 14; Length 699;
Pred. No. 2.2e-13;
8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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US-09-740-627-10

| Jaquence | Lo. Application US/09740627
| Patent No. US20020012964A1
| GENERAL INFORMATION:
| APPLICANT: NAKANISH! MAKOTO
| TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
| FILE REFREENCE: 06501-071001
| CURRENT PAPLICATION NUMBER: US/09/740,627
| CURRENT FILING DATE: 2000-12-19
| PRIOR FILING DATE: 1999-06-23
| PRIOR FILING DATE: 1999-06-23
| NUMBER OF SEQ ID NOS: 11
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.9%; Score 137.5; DB 9;
Best Local Similarity 41.3%; Pred. No. 1.5e-09;
Matches 31; Conservative 13; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 460
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-740-627-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.6%;
Matches 37; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Candida albicans
US-10-032-585-7635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 SQGDEITVG 67
                                                                                             126 QGDEITVG 133
                                                 60 QGDEITVG 67
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                                              9
WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
                             1 WTPGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 522;
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Sequence 16, Application US/10081119

Sequence 16, Application US/10081119

Publication No. US20030045491A1

SAPLICANT: Reinhard, Christoph

APPLICANT: Chan, Vivien W.

TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic

TITLE OP INVENTION: TTK in Diagnosis and STREAMENTION: TARGET IN CANCER

FILE REPERENCE: 1632.002

CURRENT APPLICATION NUMBER: US/10/081,119

CURRENT FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: 60/289,813

PRIOR FILING DATE: 2001-02-21

NUMBER: OF WINDOWS: 38

SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 313.5; DB 9; Length Pred. No. 7.8e-33; 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                    Sequence 11, Application US/09740627
Patent No. US20020012964A1
GENERAL INFORMATION:
TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
FILE REFERENCE: 06501-071001
CURRENT APPLICATION NUMBER: US/09/740,627
CURRENT FILING DATE: 1099-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.3%;
Best Local Similarity 89.7%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGDEITVG 133
                                                                                                                             OGDEITVG 68
                                                                                             QGDEITVG 67
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Best Local Similarity
Matches 61; Conserva
                                                                                                                                                                                                               RESULT 2
US-09-740-627-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-740-627-11
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LENGTH: 522
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셤 ò g Gaps

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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LOCATION: (414)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                       53 GRHPDCDLMLTHPS-ISRFHLQIRSNPSSRTFSLLDLSSVHGTWVSGRRIEPMVSVEMKE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 GRSNTCNYQLLQFT-ASYKHFRVYSVLIDDDMDFLVYCEDQSSNGTFLNHRLIGKGNSVL 136
                                                       4 GRNPACDYHLGNISRLSNKHPQIL---XXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLN-----DISTNGTWLNGQKVEKNSNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.7%; Score 86.5; DB 15; Length 474; 33.3%; Pred. No. 0.0094; tive 14; Mismatches 25; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 809, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ3 3001-01-17
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure

: LOCATION: (1)..(474)

: OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-2299
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Sequence 2299, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3%
Watches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 LSDGDILDV 145
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ORGANISM: Homo sapiens
                                                                                                                                                                                                      |: : ||
112 GETLRVG 118
                                                                                                                                                                   GDEITVG
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LENGTH: 426
     Matches
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Sequence 154547, Application US/10424599

Bublication No. US20040031072A1

GENERAL INFORMATION:
GENERAL TARGOR Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cou Yongwei
THIE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TILLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TILLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TILLE OF INVENTION: 18-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 154547
                                                                                                                                                                                                               APPLICANT: Cac, Yorgwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gladman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR SEQ ID NOS: 47374
SEQ ID NO 22674
LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 WRFGRHKSCEVVL-NGPRVSNFHFEIYQVYKIIVASXTRLVLIELQSLXDIIIXRNDPGH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|||:||
119 RNDSDESENVVFLHGKSKGLKNLLKSSASSTFSNNFRHSSNGTFLNFVSESLIRLQFTDV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.7%; Score 93; DB 15; Length 609; Best Local Similarity 23.2%; Pred. No. 0.0017; Matches 33; Conservative 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_110578C.1.pep
US-10-424-599-154547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89; DB 15;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure

: LOCATION: (1)..(609)

: OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-22674
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                                                                                                                                      Sequence 22674, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 IXERLAKNSRTILSNGDEIRIG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.5%;
32.8%;
119 NSRTILSNGDEIRIG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Gaps

25.0%; Score 84; DB 9; Length 543; 29.1%; Pred. No. 0.023; tiye 11; Mismatches 31; Indels

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1 WTFGRNPACDY------HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG 47
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                       173 ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                         48 OKVEKNSNQLLSQGDEITV 66
                                                                                                                                                              Best Local Similarity 29.19
Matches 23; Conservative
                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-437-963-156334
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                                                                                                     US-09-740-627-1
                                                                                                                                              Query Match
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NAME/KEY: SITE

1 LOCATION: (415)

2 COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE

1 LOCATION: (420)

3 CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-864-809
                                                                                                                                                                                                                                             1 WIFGRNPACDYHLGNISRLSNKHFQIL -- XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
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Pred. No. 0.022;
6; Mismatches 35; Indels
                                                                                                                                                            Score 85, DB 9, Length 426,
Pred. No. 0.013,
6, Mismatches 35, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Standard Zhou
APPLICANT: Yuan Zhu
APPLICANT: Yuan Zhu
APPLICANT: Priya Chaturvedi
APPLICANT: Xiaotong Li
APPLICANT: Xiaotong Li
TITILE OF INVENTION: FHARI, A NEW RING FINGER PROTEIN
FILE REFERENCE: GP-70668-C1
CURRENT APPLICATION NUMBER: US/09/780,525
CURRENT PILING DATE: 2001-02-09
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence I. Application US/09740627
Fatent No. US20020012964A1
GENERAL INFORMATION:
APPLICANT: Nakanishi, Makoto
TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
FILE REFERENCE: 06501-071001
CURRENT APPLICATION NUMBER: US/09/740,627
CURRENT FILING DATE: 2000-12-19
PRIOR PILING DATE: 1999-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/09780525; Patent No. US20020004223A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.3%;
34.8%;
                                                                                                                                                              ch 25.3%;
1 Similarity 34.8%;
23; Conservative
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ORGANISM: HOMO SAPIENS
                                                                                                                                                              Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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LENGTH: 664
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4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
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24.3%; Score 81.5; DB 9; Length 288;
Best Local Similarity 38.5%; Pred, No. 0.025;
Matches 25; Conservative 11; Mismatches 24; Indels
                                                              GENERAL INFOGRATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MAXAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: CCHIAI, KAINO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKI
ILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3552
LENGTH: 288
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Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.
Sequence 3552, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 VİTVĞ 277
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66 GRHPDSDIFLDDVTVSRRHAEFRLENNEFNVV------DVGSLNGTYVNREPVD--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                        Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Peb-2002
CLASSIFICATION: <university controverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                    NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acide
TYPE: amino acide
TYPE: amino acide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
23.7%; Score 79.5; DB 14;
Best Local Similarity 28.8%; Pred. No. 0.021;
Matches 21; Conservative 16; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                               ;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-193-002-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-084-843-64
; Sequence 64, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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114 SAVLANGDEVQIG 126
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 NQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
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                                        APPLICANT: Wu, Wei Mei Andrey A. APPLICANT: Wu, Wei Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERBENCE: 38-21(53221)B CURRENT APPLICATION NUMBER US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 FGRHPECHVLVDHPSVSRFHLEVRSRRRQRRITV-----TDLSSVHGTWISGRRIP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 FGRNPACD-----YHLGNISRLSNKHFQILXXXXXXLLNDIST-NGTWLNGQKVE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%; Score 80; DB 16; Length 1141; 26.3%; Pred. No. 0.18; ive 16; Mismatches 20; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
CITY: Seattle
COUNTRY: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_56010C.1.pep
US-10-437-963-156334
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(1141)
OTHER INFORMATION: unsure at all Xaa locations
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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-011-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Twardzik, Daniel R.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/10193002; Publication No. US20030135026A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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Vedvick, Thomas S.
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Best Local Similarity 26.39
Warrhes 20; Conservative
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                        SEQ ID NO 156334
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APPLICANT: MAUBLESBY, REKEE
APPLICANT: OETTINGER, Thomas
APPLICANT: REAGNESBN, Peter Birk
APPLICANT: RASHERN, SERIA
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: PLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS, M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT FILING DATE: 1998-03-30
FRIOR FILING DATE: 1997-04-02
FRIOR FILING DATE: 1997-04-02
FRIOR FILING DATE: 1997-04-04
FRIOR APPLICATION NUMBER: 60/044, 624
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SUPPLY ARE PRECEDIATION NUMBER: 60/070, 488
FRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SUPPLY ARE FREEDOMENT OF THE PROSE FROMENT OF THE PROSE
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                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                     ; Score 79.5; DB 14; Length 148;
; Pred. No. 0.021;
16; Mismatches 15; Indels 21
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                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-6
                                      LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09791171; Patent No. US20020094336A1; GENERAL INFORMATION:
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Publication No. US20040115211A1
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.8%;
Matches 21; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAVLANGDEVQIG 140
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114 SAVLANGDEVQIG 126
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Best Local Similarity
Matches 21; Conserva
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Publication No. US20040180056A1

Publication No. US20040180056A1

GENERAL INFORMATION:

APPLICANT: ORME, Ian M.

APPLICANT: ORME: Jan M.

TITLE OF INVENTION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMMU
FILE REFRERENCE: 3864-186292

CURRENT FILING DATE: 2003-01-10

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

SEQ ID NO 7
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                                                                                                                                                                               APPLICANT: ELORINOW, MALTIN
APPLICANT: ELORINOW, MALTER
TITLE OF INVENTION: UNCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: UNCLEIC ACIDS FRAGMENTS
TITLE OF INVENTION: UNRIPED FROM M. TUBERCULOSIS
TITLE OF INVENTION: UNMER: US/10/620,246
CURRENT PELIANG DATE: 1903-00-15
FRIOR PELIANG DATE: 1998-03-30
FRIOR APPLICATION NUMBER: 03/6/97
FRIOR APPLICATION NUMBER: 03/6/97
FRIOR PELING DATE: 1997-01-0
FRIOR FILING DATE: 1997-04-18
FRIOR PELING DATE: 1997-04-18
FRIOR PELING DATE: 1998-01-05
FRIOR PELING DATE: 1999-10-05
FRIOR PELING DATE: 1999-01-05
FRIOR PELING DATE: 1999-01-01
FRIOR PELING DATE: 1999-01-21
FRIOR PELING DATE: 1999-01-21
FRIOR FILING DATE: 1999-01-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-620-246-6
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENERANDS, Ida
APPLICANT: WELDINGH, Karin
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128 SAVLANGDEVQIG 140
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Best Local Similarity 28.89
Matches 21, Conservative
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PRIOR APPLICATION NUMBER: PCT/EP98/06981
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: GB 9722320.0
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PREUSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 543
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HANDO, SEIKO
APPLICANT: HANDO, SEIKO
APPLICANT: HANDO, SEIKO
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59 VLNSGDEVVFG 69
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US-09-738-626-5092
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                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                               80 GRHPDSDIFLDDVIVSRRHABFRLENNEFNVV-----DVGSLNGTYVNREPVD--- 127
                                                                                                                                                                                                   4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
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                                                                                                 23.7%; Score 79.5; DB 16; Length 162; 28.8%; Pred. No. 0.024; Live 16; Mismatches 15; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.2%; Score 78; DB 14; Length 324; Best Local Similarity 29.4%; Pred. No. 0.082; Matches 20; Conservative 19; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10185182A
Publication No. US20030017160A1
GENERAL INFORMATION:
APPLICANT: LUTTEN, Walter H.M.L.
APPLICANT: MCGOWAN, Clare H.
APPLICANT: MCGOWAN, Clare H.
APPLICANT: MCGOWAN, Alessandra
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REPERENCE: TSR 649.0 Div.1
CURRENT PLING DATE: 2002-09-04
PRIOR FILING DATE: 2002-09-04
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHKAWA, UUN
APPLICANT: BAHKAWA, HAROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WASHIYUKI
APPLICANT: HATTORI, WASHIYUKI
APPLICANT: HATTORI, WASHIKUKI
APPLICANT: HATTORI, WASHIKUKI
APPLICANT: HATTORI, WASHIKUKI
APPLICANTON NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 14509, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
       ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-332-512A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14509
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.8<sup>†</sup>
Matches 21; Conservative
                                                                                                                                                                                                                                                                                             55 NQLLSQGDEITVG 67
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304 NGDEVQIG 311
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Sequence 56100, Application US/10425114

Sequence 56100, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 56100

LENGTH: 1082
                                                                                                                                                             4 GRNPACDYHL-----GNISRLSNKHFQILXXXXXXLLNDISTNGTWL-NGQKVEKNSNQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GSNRSCNFPLNDQTISGNLCKI--KHTQ-GDGSAVAVLESMGSKGSVLVNGTHVKKNTSC 58
                                                                                                                         1 WTFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.9%; Score 77; DB 15; Length 1082; Best Local Similarity 31.0%; Pred. No. 0.44; Matches 22; Conservative 16; Mismatches 23; Indels 10
Query Match 22.9%; Score 77; DB 14; Length 543; Best Local Similarity 27.8%; Pred. No. 0.2; Matches 22; Conservative 11; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: JC-GMLE01810018D04_FLI.pep
US-10-425-114-56100
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1 WTFGRNPACDY------HLGNISRLSNKHFQILXXX-----XXXLLNDISTNGTWLNG 47
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Pred. No. 0.37;
9; Mismatches 33; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.8%; Score 76.5; DB 9; Length 459;
Best Local Similarity 30.8%; Pred. No. 0.19;
Matches 24; Conservative 14; Mismatches 27; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BOYLEN, John F.
APPLICANT: Bowers, Alex J.
TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
FITHER OF INVENTION: Serine-Threonine Kinase Member, h2520-40
FILE REFERENCE: 01017/37177A
CURRENT APPLICATION NUMBER: US/10/142,356
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 60/290,276
PRIOR PELLING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTING DATE: 2001-05-10
SEQ ID NO 6
LENGTH: 545
                                                                                                                                                                                                                                                       APPLICANT: Nakanishi, Makoto
TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
FILE REFERENCE: 06501-071001
CURRENT APPLICATION WUMBER: US/09/740,627
CURRENT APPLICATION NUMBER: PCT/JP99/03350
FRIOR FILING DATE: 1999-06-23
FRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PSELSEQ for Windows Version 4.0
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Publication No. US20030036183A1
GENERAL INFORMATION:
                                                                                                                                                              Sequence 9, Application US/09740627; Patent No. US20020012964A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 OKVEKNSNQLLSQGDEITV 66
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Best Local Similarity 29.1%;
Matches 23; Conservative
   163 HVGDVIRFG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-10-142-356-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9
LENGTH: 459
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US-10-142-356-6
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                                                                                                                                      US-09-740-627-9
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Coa Vania Baria APPLICANT: Application State APPLICANT: APPLICANT: APPLICANT: Cao Vania APPLICANT: Cao Vania Baria and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE SETERENCE: 38-21(5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 187236
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 YMFGRLDLCDFVLEHPTISRF-HAVVQFKRSGDAYLYDLGSTHGTFLNKNQVEKNTYVDL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WIFGRNPACDYHLGN--ISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.8%; Score 76.5; DB 9; Length 143; Best Local Similarity 31.3%; Pred. No. 0.051; Matches 21; Conservative 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Clone ID: PAT_MRT3847_140086C.1.pep
US-10-424-599-187236
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                    TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT PELING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PELICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR PELICATION NUMBER: UP 00/280988
PRIOR PELING DATE: 2000-04-07
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PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5092
                        TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
YOKOI, HARUHIKO
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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85 YVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNK 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10618173
Sequence 2, Application US/10618173
Publication No. US2040018603A1
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: GUO, Zijian
APPLICANT: DUNPHY, William
TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
FILE REFERENCE: CIT1350-1
CURRENT APPLICATION NUMBER: US/10/618,173
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US 60/202,028
PRIOR PILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/202,028
SPRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                               21.9%; Score 73.5; DB 9; Length 517; 25.3%; Pred. No. 0.55;
                   APPLICANT: GUO, Zijian
APPLICANT: DUNPHY, William
TITLE OF INVENTY, WILLIAM
TITLE OF INVENTY SOLISSO-1
CURRENT APPLICATION NUMBER: US/09/849,617
CURRENT APPLICATION NUMBER: US/09/99,617
PRIOR APPLICATION NUMBER: US 60/202,028
PRIOR FILING DATE: 2000-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 EIIGKGRTLPLTNNAEIAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 EIIGKGRTLPLTNNAEIAL 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 QKVEKNSNQLLSQGDEITV 66
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 25.38
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Xenopus laevis
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Xenopus laevis
US-09-849-617-2
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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US-09-738-626-3551
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                                                                                                                                                                                                                                                                                                           TYPE: PRT
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APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TFGRNPACDYHLG------NISRLSNKHFQILXXXXXXLLN--DISTNGTWLNGQ 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          22.2%; Score 74.5; DB 10;
28.8%; Pred. No. 0.11;
tive 15; Mismatches 16;
                                                                                     APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1578, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Mycobacterium tuberculosis
US-09-804-980-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09849617
Publication No. US20020086392A1
GENERAL INFORMATION:
                 ; Sequence 6, Application US/09804980; Publication No. US20030147897A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SELVK-KDYILKNGDRIVFG 128
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Matches 23, Conservative
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US-10-369-493-1578
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US-09-804-980-6
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296 HWGEPAELAHGDITLG 312
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Sequence 65407, Application US/10425114

Publication No. US20040034888A1

SEQUENCE 65407

Publication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwai

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 TMGRSPECTFVVGD-DYASGMHARVFKRGSEWFVEDLDSRNGTFVGGTRIDQ--PEQIAV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.7%; Score 73; DB 9; Length 154; Best Local Similarity 25.4%; Pred. No. 0.16; Matches 17; Conservative 19; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB4763-012-B1_FLI.pep
US-10-425-114-65407
                                                                                                                                                     APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PRILING DATE: 1999-112-16
PRIOR PILING DATE: 1999-12-16
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PARENTIN VET. 3.0
SOFTWARE: PARENTIN VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Corynebacterium glutamicum
MIZOGUCHI, HIROSHI
                                                                                         YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                            HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 GTDİRIĞ 146
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-738-626-3551
                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 163818, Application US/10437963
; Sequence 163818, Application US/10437963
; Publication No. US20040123343A1
; GRNERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: APPLICANT: APPLICANT: Wu, Wei
    APPLICANT: Wu, Wei
    APPLICANT: Wu, Wei
    APPLICANT: Barbazuk, Brad
    APPLICANT: Li, Ping
    APPLICANT: Li, Ping
    APPLICANT: Li, Ping
    APPLICANT: Li, Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Rice Nucleic Acid Molecules Associated With
    TITLE OF INVENTION: Language Construction of the Number of Second Control of the Number of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control of Second Control
APPLICANT: Lau, Jingdong
APPLICANT: Zhou, Yihuu
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
TYPE: Number OF SEQ ID NOS: 73128
TYPE: No. 56757
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US-10-425-114-56757
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US-10-437-963-163818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays
FEATURE:
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Sequence 4, Application US/10080170

Sequence 4, Application US/10080170

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: OCLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.018

FILE REFERENCE: 03495.018

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFFWARE: PATENTIN VEY: 2.1
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                                                                                                                                       4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVBKNSNQLLSQGD
                                                       S.
Query Match 20.4%; Score 68.5; DB 14; Length 843; Best Local Similarity 29.4%; Pred. No. 4.4; Matches 20; Conservative 16; Mismatches 27; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9696
                                                                                                                                                                                                                                                                                                                                                                           Sequence 9696, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Streptomyces avermitilis
US-10-156-761-9696
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Show Yihua
APPLICANT: Zhow Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(33223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:| :| : |
----DDLSNSGCFVQGLDCCLYVDAINCVSQS 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.4%; Score 68.5; DB 15; Length 376; ilarity 26.4%; Pred. No. 1.8; Conservative 19; Mismatches 29; Indels 5.
                                  4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_52888C.1.pep
US-10-424-599-233512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHEAF, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASHIYUKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 299-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13999
                                                                                                                                                                                                                                                                                                         ; Sequence 233512, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13999, Application US/10156761
Publication No. US2030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: INFEDA, HARNO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HROSHI
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                                                                                                                                                               : |:| || || :
724 LLKFFEENKEMLLSFGDSV 742
                                                               48 -- OKVEKNSNOLLSQGDEI 64
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209 CMLNSGDEVVFG 220
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ORGANISM: Glycine max
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Matches 19; Conserva
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Indels

Length 488;

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Query Match 20.1%; Score 67.5; DB 16; Best Local Similarity 32.3%; Pred. No. 3.2; Matches 21; Conservative 13; Mismatches 26;
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NAME/KEY: SITE
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| Sequence 4, Application US/10080170
| Publication No. US20040121322A9
| GENERAL INFORMATION:
| APPLICANT: COLE, S.T.
| TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
| TITLE OF INVENTION: TREATMENT OF MYCOBACTERIASES
| TITLE OF INVENTION: TREATMENT OF MYCOBACTERIASES
| FILE REFERENCE: 03495.0218
| CURRENT APPLICATION NUMBER: US/10/080,170
| PRIOR FILING DATE: 2002-06-10
| PRIOR FILING DATE: 2001-02-22
| NUMBER OF SEQ ID NOS: 652
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 4
                                                                                             3
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FILE REFERENCE: 05394.0019

CURRENT APPLICATION NUMBER: US/10/468,356

CURRENT FILING DATE: 2003-08-19

PRIOR FILING DATE: 2002-02-22

PRIOR FILING DATE: 2002-02-22

NUMBER OF SEQ ID NOS: 655

SOFTWARE: PATENTIN VOY: 3.2
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                                                                                                                                         4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
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                                            Query Match 20.1%; Score 67.5; DB 14; Length 488; Best Local Similarity 32.3%; Pred. No. 3.2; Matches 21; Conservative 13; Mismatches 26; Indels 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-468-356-4
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US-10-080-170-4
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Best Local Similarity
Matches 21; Conserv
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475 VIRLG 479
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LENGTH: 488
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US-10-080-170-4
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JS-10-080-170-4
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; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1109
                                  62
4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENDITON: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1109
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19.9%; Score 67; DB 9; Length 92; Best Local Similarity 32.7%; Pred. No. 0.57; Matches 17; Conservative 6; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                 ; Sequence 1109, Application US/09764864
; Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                 475 VIRLG 479
                                                                                                                      63 EITVG 67
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

- protein search, using sw model OM protein February 24, 2005, 15:12:40; Search time 26.1463 Seconds (without alignments) 246.555 Million cell updates/sec Run on:

US-09-936-956-19 336 1 WTFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDEITVG 67 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	313.5	93.3	821	-	A39616	protein kinase RAD
7	137.5	40.9	460	N	S58882	protein kinase Cds
m	87	25.9	159	N	A96962	FHA-domain contain
4	86.5	25.7	445	(1)	T43420	probable protein k
S	S	25.4	497	7	F83634	hypothetical prote
9	81	24.1	952	~	T18837	hypothetical prote
7	80	23.8	399	~	AC3089	
80	80	23.8	399	7	G98197	hypothetical prote
σı	79.5	23.7	162	N	D70721	hypothetical prote
10	78.5	23.4	1524	N	A96950	DNA segregation AT
11	78	23.2	1587	N	G86467	hypothetical prote
12	75.5	22.5	234	~	AF2214	hypothetical prote
13	74.5	22.2	162	~	T44758	hypothetical prote
14	74	22.0	513	Н	843941	protein kinase DUN
15	71.5	21.3	386	N	B71407	hypothetical prote
16	70	20.8	583	7	T02045	
17	69.5	20.7	157	N	S76488	hypothetical prote
18	69.5	20.7	445	N	AB2022	hypothetical prote
19	69.5	20.7	546	N	AE1899	adenylate cyclase
20	67.5	20.1	463	N	T10015	hypothetical prote
21	67.5	20.1	488	~	F86911	conserved hypothet
22	67	19.9	2897	7	B48666	prol
23	67	19.9	2938	~	T30249	
24	67	19.9	3256	~	A48666	
25	ė.	19.8	230	7	A83872	hypothetical prote
56		19.5	397	~	D83437	hypothetical prote
27		19.3	579	N	T37248	probable matrix me
28	65	19.3	598	N	T32166	hypothetical prote
29	64.5	19.2	527	N	B70700	hypothetical prote

FHA domain [import	Fha domain (homolo	Nijmegen breakage	probable ABC trans	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	probable membrane	penicillin-binding	protein C18H9.1 [i	hypothetical prote	oxi3 intron 3 prot	hypothetical prote	hypothetical prote	probable membrane	
E86579	H72046	T00393	D70986	T49879	D96904	T19167	T16191	S51457	S75331	D88188	876973	QXBY33	C90657	C85508	S52706	
7	N	0	н	~	~	N	~	~	~	7	~	н	~	~	7	
845	845	754	865	1075	468	150	431	478	749	192	210	378	426	433	604	
18.8	18.8	18.5	18.3	18.3	18.0	17.9	17.9	17.9	17.9	17.7	17.7	17.7	17.7	17.7	17.7	
63	63	62	61.5	61.5	60.5	9	9	9	9	59.5	59.5	59.5	59.5	59.5	59.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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protein kinase RAD53 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) N;Alternate names: protein P2588; protein YPL153c; SPK1 protein C;Species: Saccharomyces cerevisiae

C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A39616; S65164; S69446; S13321
R;Stern, D.F.; Zheng, P.; Beidler, D.R.; Zerillo, C.
A)C. Cell. Biol. 11, 987-1001, 1991
A;Title: Spk1, a new kinase from Saccharomyces cerevisiae, phosphorylates proteins on se A;Reference number: A39616; MUID:91117267; PMID:1899289
A;Accession: A39616

A;Residues: 1-821 <STE> A;Cross-references: UNIPROT:P22216; GB:M55623; NID:g172656; PIDN:AAA35070.1; PID:g172657 A, Molecule type: DNA

A; Experimental source: strain S288C

R;Zheng, P.; Fay, D.S.; Burton, J.; Xiao, H.; Pinkham, J.L.; Stern, D.F.
Mol. Cell. Biol. 13, 5829-5842, 1993
A;Title: SPK1 is an essential S-phage-specific gene of Saccharomyces cerevisiae that encrayerence number: A54697; WUID:93361015; PMID:8355715 A; Contents: annotation R; Purnelle, B.; Coster, F.; Goffeau, A. submitted to the Protein Sequence Database, May 1996 **Reference number: S65154

A;Accession: S65164
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-821 <PUR>
A;Experimental source: strain S288C (AB972)
A;Experimental source: strain S288C (AB972)
A;Experimental source: strain S288C (AB972)
A;Experimental source: strain S288C (AB972)
A;Experimental source: strain S288C (AB972)
A;Experimental source: strain S288C (AB972)
A;Experimental source: strain S288C (AB972)
A;Experimental source: S188C (AB972)
A;Experimental source: S69428
A;Reference number: S69428

A;Accession: S69446

A; Molecule type: DNA A; Residues: 1-821 < PUW>

A;Cross-references: EMBL:X96770; NID:g1403537; PIDN:CAA65568.1; PID:g1403556

A;Gene: SGD:RAD53; SPK1; MEC2; SAD1; MIPS:YPL153C A;Cross-references: SGD:S0006074; MIPS:YPL153C A;Map position: 161

A) Description: serine/threonine-specific protein kinase
A;Note: contains low activity as tyrosine-specific protein kinase
A;Note: contains low activity as tyrosine-specific protein kinase
A;Note: contains low activity as tyrosine-specific protein kinase
C;Superfamily: protein kinase SPK1; kinase interaction domain homology and any activity for a serine/threonine-speci
F;68-133/Domain: kinase interaction domain homology activity
F;106-466/Domain: protein kinase homology activity
F;204-213/Region: protein kinase ATP-binding motif
F;207/Active site: Lys #status predicted

us-09-936-956-19.rpr

N

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FHA-domain containing secreted protein [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum 14-Sep-2001 #text_change 09-Jul-2004 C; Accession: A96962 S; Nobling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R.; Lee, J; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. A; Reference and Comparative Analysis of the Solvent-Producing Bacterium Clost A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:097LQ0; GB:AE001437; PIDN:AAK78484.1; PID:g15023366; GSPDB:GN
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable protein kinase (BC 2.7.1.-) mekl - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe (C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 16-Aug-2004 C;Accession: T43420; T37688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:298596; PIDN:CAB11196.1; GSPDB:GN00066; SPDB:SPAC14C4.03
A;Experimental source: strain 972h-; cosmid c14C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 TIGRKDDNSIML-NEGYVSGHHARVYLRNNOYILEDLNSTNGTVLNGOKIK--SKAYIKS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
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A;Status: translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-445 cLYN>
A;Residues: 1-445 cLYN>
A;Cross-references: UNIPROT:Q10292; EMBL:Z71478; PIDN:CAA96101.1
A;Experimental source: strain 972h(-)
A;Experimental source: crain 972h(-)
A;Experimental source: drain 972h(-)
A;Experimental source: strain 972h(-)
A;Experimental 972h(-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 87; DB 2; Length 155
Pred. No. 0.001;
9; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-445 <DEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R,Lyne, M.H.
submitted to the EMBL Data Library, June 1996
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C;Superfamily: protein kinase homology
                                                                                                                           119 NSRTILSNGDEIRIG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.3%;
Matches 25; Conservative
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                                                   NSNOLLSQGDEITVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GDEİKIĞ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GDEITVG 67
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Best Local Similarity
Matches 23; Conserv
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A, Gene: CAC0504
                                              53
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A; Map position: 3
A; Introns: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2
C; Function:
C; Function:
C; Function: EC 2.7.1.-; protein kinase Cds1 [validated, MUID:98119835]; is required the pascription: EC 2.7.1.-; protein kinase cds1 [validated, mulp.) 98119835]; is required the phosphorylated and activated by S-phase arrest and activated by DNA dama C; Superfamily: protein kinase cds1; kinase interaction domain homology; protein kinase to kinase interaction domain homology «KIH»
C; Superfamily: protein kinase homology «KIN»
F; 165-433/Domain: protein kinase APP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein kinase Cds1 (EC 2.7.1.-) [validated] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004 C;Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004 R;Murakami, H.; OKayama, H. Mature 374, 817-819, 1995 Mature 374, 817-819, 1995 A;Title: A kinase from fission yeast responsible for blocking mitosis in S phase. A;Reference number: S58882; MulD:95240713; PMID:7723827
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A; Residues: 1-202, 1', 204-237, F', 239-460 < WOO>
A; Residues: 1-202, 1', 204-237, F', 239-460 < WOO>
A; Residues: 1-202, 1', 204-237, F', 239-460 < WOO>
A; Cross=references: BMBL:ALi09736; NID:95701956; PIDN:CAB52158.1; PID:g5701966; GSPDB:GN
A; Experimental source: strain 972h(-); cosmid C18B5
R; Lindsay, H.D.; Griffiths, D.J.F.; Edwards, R.J.; Christensen, P.U.; Murray, J.M.; Osma
Genes Dev. 12, 382-395, 1998
A; Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoi
A; Reference number: Z26084; MUID:98119835; PMID:9450932
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A;Cross-references: BMBL:AJ222869; NID:g2689196; PIDN:CAA11019.1; PID:g2689197
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                                                                                                                                                                                                                             66 WTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTWGTWLNGGKVEKNSNQLLS
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J.
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و
    Score 313.5; DB 1; Length 821;
Pred. No. 4e-32;
0; Mismatches 6; Indels 1.
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A;Residues: 1-60,'G',62-202,'I',204-460 <MUR2>
A;Cross-references: EMBL:X85040; NID:g794146; PIDN:CAA59410.1;
R;Mood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez,
submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Indels
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A;Cross-references: UNIPROT:Q09170; EMBL:X85040; NID:g794146
R;Murakami, H.
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; Pred. No. 1e-09;
13; Mismatches 22;
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A;Molecule type: DNA
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93.3%;
ilarity 89.7%;
Conservative (
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A;Accession: T41204
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QGDEITVG 133
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                                                                                                                                                                                                                                                                                                                                    QGDEITVG 67
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                                          Similarity
61; Conserv
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Query Match
Best Local S
Matches 61
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Best Local S:
Matches 31
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A; Cross-references: UNIPROT: QBU7W4; GB: AE008689; PIDN: AAL45129.1; PID: g17742801; GSPDB: GA; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G98197
R;Goodner, B:; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2338, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUD:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AGR_L_1057 [imported] - Agrobacterium tumefaciens (strain C58, Cere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:Q8U7W4, GB:AE007870; PIDN:AAK89105.1; PID:g15158909; GSPDB:G
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D70721
hypothetical protein Rv1827 - Mycobacterium tuberculosis (strain H37RV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 23.8%; Score 80; DB 2;
Best Local Similarity 26.7%; Pred. No. 0.022;
Matches 20; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: linear chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 NSNQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
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GESARLRDGSQINIG
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A;Molecule type: DNA
A;Residues: 1-399 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
Residues: 1-399 < KUR>
                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: AGR_L_1057
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A;Gene: Atu4335
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                                                                                                                                                                                                                                                                                                                                                                              Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Artitle: Complete genome sequence of Peeudomonas aeruginosa PA01, an opportunistic pathor A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: R83634
A; Accession: Preliminary
A; Molecule type: DNA
A; Residues: 1-497 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-952 <WILD.
A;Cross-references: UNIPROT:P46012; EMBL:Z35595; PIDN:CAA84636.1; GSPDB:GN00020; CESP:CC
A;Experimental source: clone C0166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:091751; GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AAG0347
A;Experimental source: strain PAO1
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                          65 GRSNTCNYQLLQFT-ASYRHFRVYSVLIDDDMDPLVYCEDQSSNGTFLNHRLIGKGNSVL 123
                                                                                                                                                                                                                                                                           hypothetical protein PA0081 [imported] - Pseudomonas aeruginosa (strain PA01) (Speciles: Pseudomonas aeruginosa C; Speciles: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: P83634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TFGRNPACDYHLGNISRL-SNKHFQILXXXXXXLLNDISTNGTWL--NGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 TIGRGPDNDWVLPDPERLVSSRHCTILNRDGVYYLTDTSTNGVLLVNAGHRLRRGNSEPL 88
---DISTNGTWLNGQKVEKNSNQL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypochetical protein C01G6.5 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81; DB 2; Length 952;
Pred. No. 0.042;
9; Mismatches 11; Indels
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A;Introns: 34/2; 61/2; 101/3; 195/1; 218/3; 845/3; 886/3
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A;Accession: T18837
A;Status: preliminary; translated from GB/EMBL/DDBJ
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GRNPACDYHLGNISRLSNKHFQILXXXXXLLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T18837
R;Berks, M.
submitted to the EMBL Data Library, August 1994
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Best Local Similarity 41.2%;
Matches 14; Conservative
                                                                                                                                             124 LSDGDILDV 132
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QDGETVRLG 97
                                                                                                58 LSQGDEITV 66
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A,Gene: CESP:C01G6.5
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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Fitle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A,Reference number: A86141; MUID:21016719; PMID:11130712
A,Status: preliminary
A,Molocula L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1.1587 <STO>
A;Cross-references: UNIPROT:Q9C8N3; GB:AE005172; NID:g10092383; PIDN:AAG12790.1; GSPDB:GI
C;Genetics:
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A;Cross-references: UNIPROT:Q8YS22; GB:BA000019; PIDN:BAB74968.1; PID:g17132364; GSPDB:G?
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 WIGRDRHNGICTYDKLLSRHHAAIKYVENQGF-----LLIDFQSTNGSFVNGEPVY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GRNPACDYHLGNISRLSNKHFQI---LXXXXXXLLNDIST-NGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein MLCB1788.36c [imported] - Mycobacterium leprae C.Species: Mycobacterium leprae C.Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein alr3269 [imported] - Nostoc sp. (strain PCC 7120)
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R;Parkhill, J; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, October 1997 A;Reference number: 222833
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143 QPI--ILKDGDRVRLG 156
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29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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A,Gene: alr3269
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C)Species: Clostridium acetobutylicum
C)Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C)Accession: A96590
R)Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A) Bacteriol. 183, 4832-4838, 2001
A) Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A) Reference number: A96900; MUID:21359325; PMID:21359325
A) Retus: preliminary
A) Residues: 1-1524 KMRA
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        C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70721
R;Cole, S.T; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Nationaleam, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Accession: D70721
A;Accession: D70721
A;Accession: D70721
A;Accession: D70721
A;Residues: 1-162 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q50606; GB:Z78020; GB:AL123456; NID:g3261625; PIDN:CAB01474.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q97LZ2; GB:AE001437; PIDN:AAK78388.1; PID:g15023260; GSPDB:
A;Expertimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A96950
DNA segregation ATP-ase FtsK/Spoiis (three ATPases), contains FHA domain [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WTFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.7%; Score 79.5; DB 2; Length 162;
28.8%; Pred. No. 0.0095;
ive 16; Mismatches 15; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : :|: |||: :|
128 SAVLANGDEVQIG 140
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Best Local Similarity 28.8
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 NQLLSQGDEITVG 67
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EDDQINI 177
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Best Local
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Cidate: 03. Aug-1998 #sequence_revision 03. Aug-1998 #text_change 09-Jul-2004
Cidacession: B71407
Eibevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk R.; Wedler, H.; Wedler, E.; Wambutt, R.; Weizenegger, T.; Pohl, T.W.; Terryn, N.; Giel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Mature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans, A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A;Reference number: A71400; MUID:98121113; PMID:9461215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-583 <BRA>
A;Residues: 1-583 <BRA>
A;Cross-references: UNIPROT: 049973; EMBL: U81960; NID: 92735007; PIDN: AAB93832.1; PID: 9273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: 023305; GB: Z97336; NID: 92244788; PID: e326894; PID: 92244805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Accession: T02045.
R, Brann, D.M.; Stone, J.M.; Walker, J.C.
R, Brann, to the EMBL Data Library, December 1996
A, Description: Multiple receptor-like protein kinases interact with the KI domain of
                                                                                                                                                                                                                                            ----RNLINVIDKSRNGTFINGN 110
                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase associated protein phosphatase - maize
C;Species: Zea mays (maize)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 PGSTIRVGRIVRGNEIAIKDAGISTKHLRIESDSGNWVIQDLGSSNGTLLNSNALDPETS
                                                                                                                                                                              2 TFGRNPACDYHLG------NISRLSNKHFQILXXXXXXLLN--DISTNGTWLNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.3%; Score 71.5; DB 2; Length 386; 27.8%; Pred. No. 0.26; tive 12; Mismatches 29; Indels 11
                                           DB 1; Length 513;
                                                                                                         Indels
                                       22.0%; Score 74; DB 1; Le 29.1%; Pred. No. 0.17; tive 14; Mismatches 22;
                                                                                                                                                                                                                             hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                                                                                                                                                                                                                                                                                                                                111 RLVK-KDYILKNGDRIVFG 128
                                                                                                                                                                                                                                                                                                                    49 KVEKNSNQLLSQGDEITVG
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                                Query Match
Best Local Similarity 29.1%
Matches 23; Conservative
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Best Local Similarity 27.8%
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 4COP9-4G3845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Residues: 1-386 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T02045
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F; 198-480/Domain: protein kinase homology «KIN»
F; 206-214/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P39009; EMBL:L25548; NID:g435616; PIDN:AAA16324.1; PID:g4356
R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Bd
Bubmitted to the Protein Sequence Database, July 1996
A;Reference number: 867629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
Miseidues: 1-513 - cABL>
A; Residues: 1-513 - cABL>
A; Cross-references: EMBL: 274149; NID: g14311139; PIDN: CAA98668.1; PID: g1431140; GSPDB: GNOG
A; Experimental source: strain $288C
A; Experimental source: strain $288C
B; Boskovic, J.; Salz, J.E.; Soler-Mixa, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimine submitted to the EMBL Data Library, February 1996
A; Reference number: $67406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F.
Sast 12, 107-10184, 196
A;Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerev
A;Reference number: S72094; MUID:97051597; PMID:8896274
A;Accession: S72.06
A;Accession: S72.06
A;Accession: DNA
A;Accession not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein kinase DUNI (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein D2370; protein YDL101c
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43941; S67643; $67418; S72106
F;Zhou, Z.; Elledge, S.J.
Cell 75, 1119-1127, 1993
A;Title: DUNI encodes a protein kinase that controls the DNA damage response in yeast.
A;Reference number: S43941; MUID:94084787; PMID:8261511
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A)Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64912.1; PID:g1199548
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                             'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-513 <BOS>
A;Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64912.1; PID:g1199548
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                          EMBL: AL008609; PIDN: CAA15468.1
                                                                                                                                                                                                                                                                                                                 Query Match 22.2%; Score 74.5; DB 2; Length 162; Best Local Similarity 29.2%; Pred. No. 0.042; Matches 19; Conservative 18; Mismatches 23; Indels
A;Accession: T44758
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: MIPS:YDL101c; SGD:S0002259
                                                                 A;Molecule type: DNA
A;Residues: 1-162 <PAR>
A;Cross-references: UNIPROT:032919;
A;Experimental source: cosmid B1788
C;Genetics:
A;Note: MLCB1788.36c
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A;Residues: 1-513 <ZHO>
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C,Accession: AE1899
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-546 «KUR»
A;Cross-references: UNIPROT:P94184; GB:BA000019; PIDN:BAB72700.1; PID:g17130088; GSPDB:Gr
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                adenylate cyclase (imported) - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 FIIGRLPECNLYL-PPAGVSRKHAQLVKKADGKWIIEDLGSKNGTQVN-QSIVSHPRQ-L 80
  38 GRDPSCQVVLDAMMYRMVSRRHAVVRPVASSVDSKFSWVLCDLNSANGTYLNGQRL--YG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycobacterium leprae
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein MLB1770.15c - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cole, S.T. submitted to the EMBL Data Library, August 1997 A;Reference number: 216916 A;Accession: T10015
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A;Molecule type: DNA
A;Residues: 1-463 <COL>
                                                                                       | | | | |::|
96 COELHAGDRISLG 108
                                                          67
                                                          55 NOLLSQGDEITVG
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Best Local Similarity
Matches 23; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: AE1899
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AB2022

AB2022

AB2022

Apporthetical protein alr1728 [imported] - Nostoc sp. (strain PCC 7120)

C.Species Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

A,Note: Nostocs sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C,Accession: A8-Dec-3001

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; M.; Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: AB2022

A;Accession: AB2022
                                                                                                                                                                                                                                                                                                                                                                                      S76488

hypothetical protein - Synechocystis sp. (strain PCC 6803)

hypothetical protein - Synechocystis sp.

G. Species: Synechocystis sp.

A. Variety: PCC 6803

C. Bate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

G. Accession: S76488

G. Accession: S76488

G. Accession: S. Stringo, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimgo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A.Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S76488
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <KAN>
A;Residues: 1-157 <KAN>
A;Cross-references: UNIPROT:P74513; EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA1861
A;Cross-references: UNIPROT:P74513; EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA1861
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Unne 1996
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A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| ||:| | : : :| | | : :|| 32 YIIGRSPRADIRIKSQFVSRIHAVLVRKSSDDVQAAYRIIDGDEDGQSSVNGLMINGKKV
                                                                                                              2 TFGRNPACDYHLGNISRLSNKHFQIL---XXXXXXLLNDISTNGTWLNGQKVEKNS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i Score 69.5; DB 2; Length 157;
i Pred. No. 0.18;
15; Mismatches 27; Indels 13
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20.8%; Score 70; DB 2; Length 583; 36.4%; Pred. No. 0.64; tive 7; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                     262 HWGEPAELAHGDIITLG 278
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                                                                                                                                                                                                                            ----NQLLSQGDEITVG 67
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Best Local Similarity 28.6%;
Matches 22; Conservative 1
                                                       28; Conservative
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Best Local Similarity
                             Local Similarity
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A,Molecule type: DNA
A,Residues: 1-445 <KUR>
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  Query Match
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A;Accession: T30249
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2938 <STA>
A;Cross-references: UNIPROT:Q61769; EMBL:X82786; NID:g1177527; PIDN:CAA58026.1; PID:g117
A;Experimental source: strain CBA; testis
C;Genetics
A;Gene: Ki-67
C;Keywords: cell cycle control; nucleus; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rischlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, H.D.; Gerde
J. Cell Biol. 123, 513-522, 1993
A; Title: The cell proliferation-associated antigen of antibody Ki-67: a very large, ubiq
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A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-3256 < SCH>
A, Cross-references: UNIPROT: P46013; EMBL: X65550; NID: 9415818; PIDN: CAA46519.1; PID: 94158
C, Keywords: alternative splicing; cell cycle control; nucleus; tandem repeat
F;29-91/Domain: kinase interaction domain homology < KIH>
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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A;Cross-references: UNIPROT:Q9KBZ7; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB054
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 FGRSIECDIRI-OLPVVSQRHCPIVVQEQEALLYNFSSTNPTQVNGVTIDEPVR--LRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 FGRGIECDIRI-QLPVVSKQHCKIEIHEQEAILHNFSSTNPTQVNGSVIDEPVR--LKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein BH1777 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 FGRNPACDYHLGNISRLSNKHFQILXXXXXXLL-NDISTNGTWLNGQKVEKNSNQLLSQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.9%; Score 67; DB 2; Length 3256; Best Local Similarity 30.8%; Pred. No. 10; Matches 20; Conservative 13; Mismatches 28; Indels
                      1 for cell cycle progression.
A;Reference number: Z20787; MUID:96431717; PMID:8834799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A48666; MUID: 94043435; PMID: 8227122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation antigen Ki-67, long form - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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A; Status: preliminary
A; Molecule type: DNA
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conserved hypothetical protein ML0022 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F86911
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, A;Reference number: A69909; MuID:21128732; PMID:11234002
A;Accession: F86911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <570>
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cell proliferation antigen Ki-67 - mouse

Cispecies: Mus musculus (house mouse)

Cispecies: Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

Cistacession: T30249

Ristarborg, M.; Gell, K.; Brundell, E.; Hoog, C.
J. Cell Sci. 109, 143-153, 1996

A;Title: The murine Ki-67 cell proliferation antigen accumulates in the nucleolar and he
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C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 15-Mar-2004
C;Accession: B4866
R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, H.D.; Gerde J. Cell Biol. 123, 513-522, 1993
A;Title: The cell proliferation-associated antigen of antibody Ki-67: a very large, ubiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9CDE4; GB:AL450380; NID:g13092432; PIDN:CAC29530.1; GSPDB:d
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A;Residues: 1-2897 «SCH»
A;Cross-references: EMBL:X65551
C;Reywords: alternative splicing; cell cycle control; nucleus; tandem repeat
F;29-91/Domain: kinase interaction domain homology «KIH»
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Best Local Similarity
Local 21; Conserve
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A;Status: preliminary
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B48666
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A;Cross-references: UNIPROT:P71590; GB:Z80233; GB:AL123456; NID:g3261645; PIDN:CAB02440.
A;Experimental source: strain H37Rv
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C;Accession: B70700

S;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Ritle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-598 <DUZ>
A;Cross-references: EMBL:AF022971; PIDN:AAC25839.1; GSPDB:GN00023; CESP:C31B8.8
A;Experimental source: strain Bristol N2; clone C31B8
456 FSSNRVYSYYESNIRQI-----FQMDSGFPKTLPSDLGFSVSGALRWINGHQI-----LM 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: B70700
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                         hypothetical protein C31B8.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-0c1-1999 #sequence_revision 29-0c1-1999 #text_change 29-0c1-1999 (Z,Accession: T32166 R;Du, Z.; Goela, D.; Harper, M. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid C31B8. A;Reference number: Z21129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Rv0020c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.3%; Score 65; DB 2; Length 598; Best Local Similarity 29.4%; Pred. No. 2.9; Matches 20; Conservative 11; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 49/1; 77/3; 154/1; 181/2; 479/3; 525/3; 563/1
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Matches 21; Conservative
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                                                                                               59 SQGDEITV
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83437
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yana, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Completed genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83437
A;Accession: D83437
A;Residues: 1-397 &STO.
A;Residues: 1-397 &STO.
A;Esidues: 1-397 &STO.
A;Esperimental source: strain PA01
C;Genetics:
A;Genetics:
A;Gene: PA1665
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A;Experimental source: strain N2; mixed developmental stage
C;Keywords: hydrolase; metalloproteinase
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                                                                                                                                                                                                                                                              TFGRNPA-----CDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWL-NGQKVEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 FGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI--STNGT--WLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                      1 WIFGR-----NPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-SINGTWLNGQKVEKNS 54
                                                                                                                                                           Gaps
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                                                                                            Query Match
19.8%; Score 66.5; DB 2; Length 230;
Best Local Similarity 26.4%; Pred. No. 0.66;
Matches 19; Conservative 17; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 579;
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                                                                                                                                                           27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels
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29.4%; Pred. No. 2.8;
tive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
19.5%; Score 65.5; DE
Best Local Similarity 28.0%; Pred. No. 1.6;
Matches 21; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.4%;
Matches 20; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 NSNQLLSQGDEITVG 67
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                                                                                                                                                                                                                                                                                                                                                                                            PERLSHGDRLSL 96
                                                                                                                                                                                                                                                                                                                                                    55 NQLLSQGDEITV
C;Genetics:
A;Gene: BH1777
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Gordon, Solroyd, S.

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63 EITVG 67

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C;Accession: T00393

**Simatesura, S.; Tauchi, H.; Nakamura, A.; Kondo, N.; Sakamoto, S.; Endo, S.; Smeets, D.; Nature Genet. 19, 179-181, 1998

**Ature Genet. 19, 179-181, 1998

**Afitle: Positional cloning of the gene for Nijmegen breakage syndrome.

**A;Reference number: Z14144; MUID:9828099; PMID:9620777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 8q21
A;Introns: 13/1, 57/3, 107/2, 160/3; 195/2, 234/3; 299/2; 332/1; 375/2, 466/2; 615/3; 63
C;Superfamily: human Nijmegen breakage syndrome protein NBS1
C;Keywords: DNA repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ABC transporter Rv1747 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: D70986
B;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atlile: Declipharing the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295997; PMID:9634230
A;Accession: D70986
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:065934; GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CAB09333
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: Mycobacterium tuberculosis probable ABC transporter Rv1747; ATP-binding
                                                                                                                                                                                                                     N;Alternate names: cell cycle regulatory protein p95
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:060934; EMBL:AB013139; PIDN:BAA28616.1
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Pred. No. 9.1;
7; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T49879
hypothetical protein T211.110 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 LKDNSKYGTFVNEEKMONGFSRTLKSGDGITFG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 INDISTNGTWINGQKVEKNSNQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.3%; Score 61.5; 44.8%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 STNGTWLNGOKVEKNSNQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                              Nijmegen breakage syndrome protein NBS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.5%;
ilarity 39.4%;
Conservative
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|||::: |
481 SNQVVALG 488
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Best Local Similarity
Matches 13; Conserv
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hes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T00393
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                                                                                                                                                                             FHA domain [imported] - Chlamydophila pneumoniae (strain J138)

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Accession: B86579
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: B86579
A;Accession: B86579
A;Residues: 1-845 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-845 <ARN.
A; Residues: 1-845 <ARN.
A; Cross-references: UNIPROT: Q9Z7J3; GB.AE001652; GB.AE001363; NID:g4376997; PIDN: AAD1885
A; Experimental source: strain CW1029
B; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome Sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID: 20150255; PMID: 10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q927J3; GB:BA000008; NID:g8979084; PIDN:BAA98919.1; GSPDB:GN
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0712
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A,Molecule type: DNA
A,Residues: 1-845 - KREA
A,Fosidues: 1-845 - KREA
A,Cross-references: GB:AE002167; GB:AE002161; NID:g7188971; PIDN:AAF37929.1; PID:g718897
A,Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Chlamydophila pneumoniae (strains CWL029 and
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H72046
Fha domain (homolog to adenylate cyclase) - Chlamydophila pneumoniae (strains CWL029 C)
Fha domain (homolog to adenylate cyclase) - Chlamydophila pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C; Accession: H72046; A81650
Nature Genet. 21, 385-389, 1999
Nature Genet. 21, 385-389, 1999
A; Ffebrence number: A72000; MUID: 99206606; PMID: 10192388
A; Accession: H72046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WTFGRNP-ACDYHLGNISRLSNKHFQI-LXXXXXXLLNDI-STNGTWLNGQKVEK----N 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.8%; Score 63; DB 2; Length 845; Best Local Similarity 29.4%; Pred. No. 7.6; Matches 20; Conservative 19; Mismatches 21; Indels
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SNOVVALG 488
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Best Local Similarity
Matches 20; Conserva
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| :|
514 VIRLG 518
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A;Gene: CPn0712; CP0034
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A; Molecule type: DNA
A; Residues: 1-150 <WIL>
A; Cross-references: UNIPROT: Q9U3Q2; EMBL: Z50109; PIDN: CABS4192.1; GSPDB: GN00020; CESP: CO:
A; Experimental source: clone C09H10
C; Genetics:
A; Gene: CESP: C09H10.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT:Q19846; EMBL:U49829; NID:g1203924; PID:g1203931; PIDN:AAA9338(
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:Q06001; EMBL:U19027; NID:g609363; PID:g609364; GSPDB:GN00012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:F27D9.8
A;Introns: 8/1; 52/3; 74/1; 96/1; 128/2; 149/3; 199/2; 255/3; 297/3; 319/3; 350/3; 390/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 FGREKKVCHITFDPHAARVSRI---HASIEMGDEGLFFTDKSKEGTEINGTRLKQSSQEL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 FGR-NPAC----DYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F27D9.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: Ti6191
R;Bentley, D.
R;Bentley, D.
Submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid F27D9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N'Alternate names: hypothetical protein L8083.1
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 15/1; 58/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C09H10.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YLR238w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 17.9%; Score 60; DB 2; Length 431; sal Similarity 36.7%; Pred. No. 8.9; 11; Conservative 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hallsworth, K. submitted to the EMBL Data Library, December 1994 A;Description: The sequence of S. cerevisiae cosmid 8083. A;Reference number: S51443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: MIPS:YLR238w
A;Cross-references: SGD:S0004228
A;Map position: 12R
C;Keywords: transmembrane protein
F;455-471/Domain: transmembrane #status predicted <TVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T16191
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                              Match 17.9%; Score 60; DB 2 Local Similarity 27.1%; Pred. No. 2.8; es 19; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 ISTNGTWINGQKVEKNSNQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 LSQGDEITVG 67
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Matches 11; Conserv
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A; Residues: 1-478 <HAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S51457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S51457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable membrane protein, containing FHA domain [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: D96904 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R. Jacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q97N03; GB:AE001437; PIDN:AAK78023.1; PID:g15022857; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                             Ľe
                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: ATSP:T211.110
A,Map position: 5
A,Introns: 411/2; 456/2; 504/3; 608/1; 731/3; 768/3; 786/1; 822/3; 865/3; 895/3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49879
S;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T49879
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-1075 <BEV>
A;Gross-references: UNIPROT: Q9LY20; EMBL: ALI63912; GSPDB:GN00063; ATSP:T2II.110
A;Experimental source: cultivar Columbia; BAC clone T2II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tigl67

Hypothetical protein C09H10.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19167
R;Ainscough, R.
Submitted to the EMBL Data Library, July 1995
A;Reference number: Z19082
A;Accession: T19167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.0%; Score 60.5; DB 2; Length 468; 31.3%; Pred. No. 8.4; Live 11; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WTFGRNPA---CDYHLGNISRLSNKHFQILXXXXXLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61.5; |
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 18.3%;
1 Similarity 23.5%;
24; Conservative 1
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IRNGDTI 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: D96904
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CAC0036
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----GGNIGNGQKAMRNKNGGRNQG 130

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5 RNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQG
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C;Species Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Accession: D8848
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99669613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                   penicillin-binding protein 1B mrcB - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1710
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75331
R;Kaneko, T; Sato, S.; Kotani, H.; Tānaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75331
A; Accession: S75331
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A; Ascession: S75331
A; Ascession: S75331
A; Ascession: S75331
A; Residues: 1-749 cKAN>
A; Residues: 1-749 cKAN>
A; Cross-references: UNIPROT:P73218; EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BAA1724
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
A; Genetics:
C; Superfamily: penicillin-binding protein
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A;Note: similar to E. faecium initiation factor (IF-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GRNPACDYHLGNISRLSNKHFQILXX----XXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
                                                                                                                                                                                    67
                                                                                             Gaps
                                                                                                                                                  14 GNI-SRLSNKHFQILX---XXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGDEITVG
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                        1; Score 60; DB 2; Length 478;
1; Pred. No. 10;
15; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 60; DB 2; Length 749
; Pred. No. 16;
15; Mismatches 26; Indels
                                  17.9%;
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Best Local Similarity 27.9%;
Matches 19; Conservative 1
                                                           1 Similarity 30.5% 18; Conservative
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Matches 15; Conservative
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|120 HGDEITLG 127
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A;Molecule type: DNA
A;Residues: 1-192 <STO>
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Best Local S:
Matches 18
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using	2005,
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- protein search	February 24
OM protein	Run on:

(without alignments)
273.851 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-936-956-19 336 1 WTFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDEITVG 67

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues

1612378 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOUTHER		
Result No.	Score	Query Match	Query. Match Length	DB	ID	Description	
1	313.5	93.3	821	-	RA53 YEAST	P22216 Baccharomyc	nyc
7	313.5	93.3	821	~	Q6B1 <u>S</u> 1	Q6b1s1 saccharomyc	nyc
Э	273.5	81.4		~	Q6FK01	candida	gla
4	234	9.69	837	~	Q75CE9	ashbya	980
'n	233.5	69.5	813	N	Q6CKF2		nyc
9	171	50.9	751	~	Q6BUB2	_	Vce.
7	137.5	40.9	204	~	Q683Z9	Q683z9 schizosaccl	cch
80	137.5	40.9	460	-	CDS1 SCHPO	Q09170 schizosacch	cch
6	116	34.5	503	~	Q902 <u>Y</u> 5	Q90zy5 brachydanio	nio
10	115	34.2	868	~	Q6C079	•	. 11
11	112	33,3	503	~	Q803E2	_	nio
12	105.5	31.4	504	7	Q87PU0	vibrio	para
13	104.5	31.1	398	~	Q87HC2	vibrio	para
14	100.5	29.9	359	~	Q981K6	rhizobi	11
15	66	29.2	626	~	Q6P256	Q6p256 xenopus tro	tro
16	98.5	29.3	460	~	Q89P85	_	qoz
17	95	28.3	1029	~	Q8DJ88		200
18	93.8	27.8	567	0	Q9FWA0	Q9fwa0 arabidopsis	sis
19	93.5	27.8	585	~	Q9M8A0	Q9m8a0 arabidopsis	sis
20		27.5	443	7	Q6BH59	_	yce
21	91	27.1	374	~	QBD6T0	_	uln
22	91	27.1	434	~	Q7MDP1	Q7mdp1 vibrio vuln	uln
23	89.5	26.6	712	~	Q7SEK0	Q7sek0 neurospora	ra
24	89	26.5	398	~	Q761W8	Q761w8 entamoeba	a H
25	87.5	26.0	436	~	Q6LUB6		ter
56	87	25.9		7	097LQ0	Q971q0 clostridium	ium
27	86.5	25.7	44	-	MEK1_SCHPO		cch
28	٠	25.4	49	~	Q917 <u>5</u> 1	Q9i751 pseudomonas	nas
29	85	25.3		-	CHFR HUMAN	-	ien
30	85	25.3	674	N	Q6MQJ2	Q6mqj2 bdellovibri	bri
31	84	25.0	346	~	Q7UIF2	Q7uif2 rhodopirell	ell

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ALIGNMENTS

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ž	Nature 307:1	:T) COT-60:						

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InterPro; IPR000253; FHA.

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InterPro; IPR000253; FHA.

InterPro; IPR000259; Kinase like.

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PDB; 1K3N; NMR; A=14-164.

PDB; 1K3O; NMR; A=14-164.

PDB; 1K3O; NMR; A=549-730.

GermOnline; 144135; ---

SGD; SO00066074; RAD53.

GO; GO:0005634; C:nucleus; IDA.

GO; GO:0004712; F:protein threonine/tyrosine kinase activity; IDA.

GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . .; IGI.
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FHA 2.
ATP (By similarity).
ATP (By similarity).
Proton acceptor.
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DOMAIN 601 664
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BINDING 227 227
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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X Kim E.M., Jang Y.K., Park S.D.;

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In E.M. Jang Y.K., Park S.D.;

Saccharomyces cerevisiae, is dependent upon Rad53 kinase.";

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In Saccharomyces cerevisiae, is dependent upon Rad53 kinase.";

In Saccharomyces cerevisiae, is dependent upon Rad53 kinase.";

In Saccharomyces cerevisiae, is dependent upon Rad53 kinase.";

In Programmer Via S-phase checkpoint as well as G1 and G2 DNA damage checkpoints. Phosphorylates proteins on serine, threonine, and tyrosine. Prevents entry into anaphase and mitotic exit after DNA damage via regulation of the Polo Kinase CDC5. Seems to be involved in the phosphorylation of RPH1.

--- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

--- SIMELARITY: Belongs to the Ser/Thr protein kinase family.

--- SIMILARITY: Contains 2 FHA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                  PHÖSPHORYLATION.
MEDIATNE=20131667; PubMed=10562568; DOI=10.1093/emboj/18.22.6561;
MEDIATNE=20131667; PubMed=10562568; Marini F., Lopes M., Plevani P., Romano A., Di Fiore P.P., Folani M.;
"Activation of Rad53 kinase in response to DNA damage and its effect in modulating phosphorylation of the lagging strand DNA polymerase.";
EMBO J. 18:6561-6572(1999).
                                                                                                                                                                                                                                  MEDLINE=20018334; PubMed=10550056; DOI=10.1126/science.286.5442.1166; Sanchez Y., Bachant J., Wang H., Hu F., Liu D., Tetzlaff M., Elledge S.J.;
Elledge S.J.;
"Control of the DNA damage checkpoint by chkl and rad53 protein kinaese through distinct mechanisms.";
                                                     MEDLINE=95047382; PubMed=7958905; Allen J.B., Zhou Z., Siede W., Friedberg B.C., Elledge S.J.; Thou Z., Siede W., Friedberg B.C., Elledge S.J.; The SADI/RAD53 protein kinase controls multiple checkpoints and DNA damage-induced transcription in yeast."; Genes Dev. 8:2401-2415(1994).
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NMR; A=573-730.
NMR; A=573-730.
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1 IPHQ; NMR; A=573-730.
1 IFHR; NMR; A=573-730.
1 IG3G; NMR; A=1-164.
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PIR; PDB; PDB; PDB; PDB;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 WIFGRNPACDYHLGNISRLSNRHFQILLGEDGNLLLNDISTNGTWLNGQRVEKNSNQLLS 125
                                                                                                                                                   1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WIFGRNPACDYHLGNISRLSNKHPQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F., Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A., Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Kinase; Serine/threonine-protein kinase; Transferase
821 AA; 91934 MW; AAB353DC7DF68119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LaBaer J.;

"Creation of the YELX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

-i SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AV693009; AAT93028.1;

SGD; S000006074; RADS3.

GO; GO:0005224; F.ATP binding; IEA.

GO; GO:0004713; F.protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F.protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.3%; Score 313.5; DB 2; Length 821;
89.7%; Pred. No. 7e-32;
ive 0; Mismatches 6; Indels 1;
                                                             93.3%; Score 313.5; DB 1; Length 821;
89.7%; Pred. No. 7e-32;
tive 0; Mismatches 6; Indels 1;
                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            821 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00240; FHA, 2.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PSS0011; PHA DOMAIN; 2.
PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000253; FHA.
InterPro; IPR000253; FHA.
InterPro; IPR000719; Winase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008290; Ser_thr_pkinase.
InterPro; IPR008249; Ser_thr_pkinase.
InterPro; IPR008245; Tyr_pkinase.
Ffam; PF00498; FHA; 2.
Pfam; PF00498; PHA; 2.
ProDom; PP0000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Conservative
                                                                                                        61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                               QGDEITVG 133
                                                                                                                                                                                                                                       60 QGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                  126
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Best Local 8
                                                               Query Match
                                                                                   Local
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                        STRAND
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TURN
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Narck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Royer B., Fahread C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zaniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
M. "Genome evolution in yeasts.";
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R InterPro; IPR000279; From an interpro; IPR0000719; From Extense like.

R InterPro; IPR000179; Proc kinase.

R InterPro; IPR000179; Proc kinase.

R InterPro; IPR0008271; Ser_thr_pkin_AS.

R InterPro; IPR000894; SMAD FHA.

R InterPro; IPR000894; SMAD FHA.

R PF0000001; Proc kinase.

R Propom, PD0000001; Proc kinase; 1.

R MART; SM00240; FA, 2.

R SMART; SM00240; FA, 2.

R SMART; SM00240; FTKc; 1.

R SMART; SM00191; TrKc; 1.

R PROSITE; PS50001; FRA DOWAIN; 2.

R PROSITE; PS50011; PROTEIN KINASE DOW; 1.

R PROSITE; PS50011; PROTEIN KINASE DOW; 1.

R PROSITE; PS5011; PROTEIN KINASE ST; 1.

R PROSITE; PS01019; PROTEIN KINASE ST; 1.

R PROSITE; PS01019; RADBE SEATH CHINASE ST; 1.

R PROSITE; PS01019; PROTEIN KINASE ST; 1.

R PROSITE; PS01019; PROTEIN KINASE ST; 1.
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                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome M complete sequence.
ORFNames-CAGLOW0223139;
Candida glabrata CBS138.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 430:35-44(2004).
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; CR380959; CA662419.1; -.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004713; F:Protein exine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.4%; Score 273.5; DB 2 ilarity 77.9%; Pred. No. 1.1e-26; Conservative 3; Mismatches 11
767 AA
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ORFNames=KLLAOF11143g;
Kluyveromyces lactis NRRL Y-1140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                            Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||:||
QGDEISVG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 QGDEITVG 67
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                            SEQUENCE FROM N.A. STRAIN=NRRL Y-1140;
                                                      NCBI_TaxID=284590;
                                                                                                        Genolevures;
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Q6BUB2;
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Q6BUB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces lactis.
                                                                                                                                                                                                                                                                                                                                                                                          R GO; GO; U00488 ; F; PICCELIN GMINO GCIG PROSPHOLYJACION; LEA.

R INTERPRO; IPRO1009; Kinase like.

R INTERPRO; IPRO1009; Kinase like.

R INTERPRO; IPRO1009; Ser_thr_pkinase.

R INTERPRO; IPRO02271; Ser_thr_pkinase.

R INTERPRO; IPRO0884; SMAD FHA.

R INTERPRO; IPRO0884; SMAD FHA.

R INTERPRO; IPRO0884; FYT_pkinase.

R PFEAM; PRO0699; PKINASE.

R PROMOF, PRO00001; PROCE Kinase; 1.

R MART; SM00240; FHA; 2.

SMART; SM00240; FHA; 2.

R SMART; SM00191; TYRC; 1.

R SMART; SM00191; TYRC; 1.

R R PROSITE; PS50006; FHA DOMIN; 2.

R PROSITE; PS50011; PROTEIN KINASE ATP; 1.

R PROSITE; PS5011; PROTEIN KINASE ST; 1.

R PROSITE; PS5011; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Serime(threonine-protein kinase; Transferase.

O SEQUENCE 837 AA; 93517 MW; DDB15B7553948627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WIFGRN-PACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Bremothecium.
                                                                                                                                                                                                                                                                                                                                             GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                              Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AE016816; AAS51368.1; -.
HSSP; P22216; 1K3Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.6%; Score 234; DB 2; Length 837;
66.7%; Pred. No. 1.7e-21;
tive 6; Mismatches 15; Indels
                                                                                                                                                                                                                                          STRAIN=ATCC 10895;
Brachat S., Voegeli S.E., Dietrich F.S., Lerch A., Gaffney
Philippsen P.;
                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  813 AA.
                                                                            837 AA.
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 105-JUL-2004 (TrEMBLrel. 27, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                           PRELIMINARY;
                                                                                        Q75CE9;
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 GOGDEITVG 161
||||||||||||||||QGDEITVG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                      ORFNames=ACR142W;
                                                                                                                                                                                                        NCBI_TaxID=33169;
                                                                                                                                                                                                                                                                                                                       HSSP; P22216
AGD; ACR142W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6CKF2;
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                                                                            Q75CE9
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ID 06
AC 06
DT 25
DT 25
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                                                                                                                                                                                                                                                     Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aagle M., Anthouard V., Babour A., Barbe V.,
A Goffard N., Frangeul L., Aagle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bloykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Nicaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
A Nicaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Seniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
A Wincker P., Souciet J.L.;
T. "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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SMART; SM00240; FHA; 2.
SMART; SM00240; FHA; 2.
SMART; SM00219; TYRC; 1.
SMOSITE; PS50010; FHA DOMAIN; 2.
PROSITE; PS50010; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serine, threenine-protein kinase; Transferase.
SEQUENCE 813 AA; 91482 MW; 949935699288789E CRC64;
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; CR382126; CAG98295.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.5%; Score 233.5; DB 2; Length Best Local Similarity 60.3%; Pred. No. 1.9e-21; Matches 41; Conservative 13; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    751 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000253; FHA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR007290; Ser Ehr pkinase.
InterPro; IPR008271; Ser Ehr pkin AS.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
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                                                                                                                                                                                                                                      Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., March C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne B., Backaten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye E., Fairhead C., Perry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski N., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Wincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WIFGRNPACDYHLGNISRLSNKHFQILXXXXXXLL--NDISTNGTWLNGQKVEKNSNQLL 58
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SMART; SM00240; FHA; 2.
SMART; SM00220; S.TKC; 1.
SMART; SM00219; TVrK; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
PROSITE; PS50011; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                            Eukaryottina; Saccharomycottes; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; CR382135; CAG86283.1; -. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0004671; F:ATP binding; IEA. GO; GO:00046713; F:protein-tyrosine kinase activity; IEA. GO; GO:0004713; F:protein-tyrosine kinase activity; IEA. GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.9%; Score 171; DB 2; Length 751; 50.7%; Pred. No. 2.6e-13; ive 9; Mismatches 23; Indels
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last anotation update)
Similar to sp|P22216 Saccharomyces cerevisiae YPLI53c SPK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       751 AA; 85411 MW; EF8A15F56A788346 CRC64;
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InterPro; IPR011009; Kinase like.
InterPro; IPR011009; Kinase like.
InterPro; IPR000139; Prot kinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00408; FHA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wincker P., Souciet J.L.;
"Genome evolution in yeasts.";
Nature 430:35-44(2004).
                                                                (Fragment).
ORFNames=DEHAOC13211g;
Debaryomyces hansenii CBS767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 50.7 tes 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                          STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CBS767;
                                                                                                                                                                                                                          Genolevures
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요
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60 WRFGRHKSCEVVL-NGPRVSNPHPEIYQGHRNDSDESENVVFLHDHSSNGTFLNFERLAK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Evolutionary conservation of a splice variant of the Cds1/Chk2 kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase cds1 (EC 2.7.1.37) (Checkpoint kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A kinase from fission yeast responsible for blocking mitosis in S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., FUNCTION, INTERACTION WITH RAD26, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restricted to its regulatory domain.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ783838; CH104269.1;
GO; GO:0016301; F:kinase activity; IEA.
InterPro; IPR000253; FHA.
InterPro; IPR001009; Kinase like.
InterPro; IPR008984; SMAD_FHA.
FILE PROSS SERVED FOR THE PROSS SERVED FOR THE PROSS SERVED FOR THE PROSS SERVED FOR THE PROSS SERVED FEAR.
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MEDLINE=95240713; PubMed=7723827; DOI=10.1038/374817a0;
Murakami H., Okayama H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 204 AA; 23162 MW; 85FC79F7553B632D CRC64;
                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                              Last annotation update)
                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 AA.
    204 AA
                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 NSRTILSNGDEIRIG 133
                                                                                25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 NSNQLLSQGDEITVG 67
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896;
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Q09170; 042642;
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                                                                                                                                                                                                                        Cds1 kinase.
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PD000001; Prot_kinase; 1.
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                                                                                                                                                                                                                                                                                             MACHOLINE-ZIRAGAGO, PUDRED. LUGBURATURE/ZA,

WOOD V., GWIlliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

By Source J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA BOOKE K., Brown D., Brown S., Chilliangworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Collins M., Connor R., Cronin B., Davis P., Feltwell T., Fraser A.,

Rollroyd S., Honnbby T., Howarth S., Huchel E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Laather S., McDonald S., McLean J.,

RA Johney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Allork K., Taylor K., Taylor K., Sauders B., Stevens K.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Taylor K., Taylor K., Taylor K., Muller S.,

RA Paylor K., Taylor K., Taylor R., Walsh S.V., Warren T.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.,

RA Dominguez A., Revuelta J.L., Moceno S., Armstrong J., Forsburg S.L.,

RA Sanchez W., Ussery D., Barrell B.G., Nurse P.;

RA Sanchez W., Ussery D., Barrell B.G., Nurse P.;

RA Sanchez B.M., Rochet W., Gallardin C., Tallada V.A., Gazon A., Thode G.,

RA Sanchez W., Wasery D., Barrell B.G., Nurse P.;

Ra Sanchez W., Wasery D., Barrell B.G., Nurse P.;

Ra The genome sequence of Schizosaccharomyces pombe.";

Rature 415:871-880(2002).

C checkpoint system. It is responsible for blocking mitosis in the Splanae. It monitors DNA synthesis by interacting with DNA while man in the DNA with DNA while man be and a signal to block the onset of mitosis while man be and a signal to block the onset of mitosis while man be and a signal to block the onset of mitosis while man be and a signal to block the onset of mitosis while man be and a signal to block the onset of mitosis while man be and a signal to block the onset of m
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SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
                                              Lindsay H.D., Griffiths D.J.F., Edwards R.J., Christensen P.U., Lindsay H.D., Griffiths D.J.F., Edwards R.J., Christensen P.U., Murray J.M., Osman F., Walworth N., Carr A.M.; "S-phase-specific activation of Cds1 kinase defines a subpathway the checkpoint response in Schizosaccharomyces pombe."; Genes Dev. 12:382-395(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              while DNA synthesis is in progress.
CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SUBUNIT: Interacts with rad26.
                                                                                                                                                                                                                                                                                    MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, 000534; 1JOW.
GeneDB_SPombe; SPCC18B5.11c; -.
InterPro; IPR0100253; FHA.
InterPro; IPR01009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser Lhr pkin AS.
InterPro; IPR002290; Ser Lhr pkin AS.
InterPro; IPR002290; Ser Lhr pkinase.
InterPro; IPR002394; SWAD FHA.
InterPro; IPR01245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 FHA domain.
                             MEDLINE=98119835; PubMed=9450932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ222869; CAA11019.1; -. BEMBL; AL109736; CAB52158.1; -. PIR; S58882; S58882. HSSP; Q00534; 1JOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X85040; CAA59410.1; -.
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Pfam; PF00069; Pkinase; 1.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WTFGRNPACDYHLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNGQKVEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WTFGRNPACDYHLGN-----ISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00498; FHA; 1.
Pfam; PF0069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00240; FHA; 1.
SMART; SM00200; STKC; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS01008; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 503 AA; 56699 MW; BC01BF3D8E4CEC71 CRC64;
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                                                                                                                                                                                              Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
R -> G (in Ref. 1).
F -> C (in Ref. 1).
W, 4CEB963D3376DB54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 460;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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40.9%; Score 137.5; DB 1;
Best Local Similarity 41.3%; Pred. No. 3.6e-09;
Matches 31; Conservative 13; Mismatches 22;
                                                                                                        PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Cell cycle; Phosphorylation;
Serine/threonine-protein kinase; Transferase.
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SMART; SM00240; FHA; 1.
SMART; SM00220; S TKC; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                FHA.
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1181
1181
1196
238
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NCBI TaxID=7955;
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Best Local Similarity 34.2%; Pred. No. 6.4e-06; , , Matches 25; Conservative 15; Mismatches 27; Indels
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91 YSFGRDKRCDYSFSNSILKKSPYFNTYSKKHPRIFRDENLVYLEDLSGNGTWVDDEKLGN 150
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A defontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthourd V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykaaten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Laminead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyer P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Ottas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T "Genome evolution in yeasts.";
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-2004) to the Ser/Thr protein kinase family.

Result (Sas132) CAG73745.

Result (Sas132) CAG73745.

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SMART; SM00220; S TKC; 1.
SMART; SM00219; TYRC; 1.
RM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 898 AA; 100328 MW; 8C648FB95899D28E CRC64;
                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to DEHAOC13211g Debaryomyces hansenii.
ORFNames-YALIOF27093g;
Yarrowia lipolytica CLIB99.
Bukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                           151 GKQSLLSNNSVIAL 164
                                                                                      53 NSNQLLSQGDBITV 66
                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Length 898;

DB 2;

Score 115;

34.2%;

Query Match

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=AB: TISSUB=Whole body;

MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

AL staubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zebebrg B., Buetow K.H., Schamen C.M., Schuler G.D.,

Altschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A plachul R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wckernan R.J., Malke J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Myting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rodrestion and initial analysis of more than 15,000 full-length human
ä
                                                                                                                82 WTFGRAGSANFVVARKARLSKIHFIVEHTGGTKQRAGTVVIRDVSLNGTSVNGRYLGRGN 141
                                                                    1 WTFGRNPACDYHLGNISRLSNKHFQI-----LXXXXXXLLNDISTNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=zgc:55865;
Brachydanio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
6; Gaps
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GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

InterPro; IPR000253; FHA.

InterPro; IPR001019; Kinase like.

InterPro; IPR000719; Prot Kinase.

InterPro; IPR002209; Ser Thr_pkinase.

InterPro; IPR008271; Ser Thr_pkinase.

InterPro; IPR008271; Ser Thr_pkinase.
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--- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC044519; AAH44519.1; --
HSSP; P49137; INXK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Pfam; PF00069; Pkinase; 1.
ProDom; PD00001; Proc kinase; 1.
SMART; SM00240; FHA; 1.
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STRAIN=AB; TISSUE=Whole body;
Strausberg R.;
                                                                                                                                                                                                                                                                         SALLQNGDVITVG 154
                                                                                                                                                                                                                         55 NOLLSQGDEITVG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHK2 checkpoint homolog.
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Hypothetical protein VPA1043
                             OrderedLocusNames=VPA1043;
                                                                                          Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mlr2358 protein.
                                                                                                                NCBI_TaxID=670,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q98IK6
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      셤
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                                                                                                                                                                                                                                                                  1 WTFGRNPACDYHLGN-----ISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GRNPACDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQGD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-RIMD 2210633 / Serotype O3:K6;

STRAIN-RIMD 2210643; Describe O3:K6;

MEDLINE-22508454; DubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

MEDLINE-22508464; DubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

MAKINO K., Oshima M., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                 Gaps
SMART; SM00220; S_TKC; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine/Chreonine-protein kinase; Transferase.
SEQUENCE 503 AA; 56657 MW; 351A24EA5BBAF8D5 CRC64;
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                                                                                                                                                    33.3%; Score 112; DB 2; Length 503; 31.1%; Pred. No. 8.4e-06; tive 11; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome; Hypothetical protein.
SEQUENCE 504 AA; 55469 MW; 2F96C75A4F83648E CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 AA
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PROSITE; PS50006; FHA DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q96EP1; 1LGQ.
InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD_FHA.
Ffam; PF00498; FHA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP005078; BAC59674.1; -. HSSP; Q96EP1; 1LGQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein VP1411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                          151 GKOSLLGNNSVIAL 164
                                                                                                                                                                                                                                                                                                                               53 NSNQLLSQGDEITV 66
                                                                                                                                                                           Local Similarity 31.1 les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=VP1411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio parahaemolyticus.
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VVSLG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=670;
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01-JUN-2003 (
01-JUN-2003 (
01-MAR-2004 (
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                                                                                                                                                      Query Match
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Q87HC2
ID Q87HC
AC Q87HC
DT 01-JU
DT 01-JU
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB PPU OB 
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2 TFGRNPACDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWLNG--QKVEKNSNQLL 58
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                                                                                                                                                                                             STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739; DOL=10.1016/S0140-6736(03)12659-1;
MAKINO K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakamo M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 398;
Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP005037; BAC62366.1; -.
InterPro; IPR000253; FHA.
InterPro; IPR00894; SNAD_FHA.
SMART; SM00240; FHA; 1.
SMART; SN00240; FHA; 1.
COMPLETE, PSS0006; FHA DOMAIN; 1.
COMPLETE PSS0006; FHA MW; 419A55457EB4D173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39374 MW; 36732CCBB6AB7DD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 31.1%; Score 104.5; DB 2; Similarity 33.3%; Pred. No. 6.2e-05; 23; Conservative 16; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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InterPro; IPR008984; SWAD_FHA.
Pfam; PF00498; FHA; 1.
SWART; SW00240; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP002999; BAB49510.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=mlr2358;
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93 SHGDTVALG 101
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Gaps

36;

4; Mismatches

Conservative

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26;
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Q89P85;
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Q8DJ88
Matches
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                                                                                                                                                                                                                                                                                                                                             Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Nausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A ploking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldon M.F., Carnhori P., Frange C.,
A Brownstein M.J., Usdin T.B., Toobhyuki S., Carnhori P., Frange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
                                       9 CDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVG 67
                                                     35 CDWTLSDPDKFISGRHCEIRYQAGTFWLHDVSRNGTFVNGSSQRNNAPHRLTQGDRLLIG 94
            Gaps
                                                                                                                                                                                                                            Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; DB 2; Length 626; Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0000151; Cubiquitin ligase complex; IEA.
GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO:0008270; F:zinc ion binding; IEA.
GO:0016567; P:protein ubiquitination; IEA.
            25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S. Gerhard D.S.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; P222A6; 1K3O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein MGC75959.
; Pred. No. 0.00018; 14; Mismatches 25
                                                                                                                                   626 AA
                                                                                                                                                          -JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IPR008984; SMAD_FHA. ; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.5%;
38.2%;
ilarity 33.3%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
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                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Best Local Similarity
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
                                                                                                                                                                                                                Name=MGC75959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro
                                                                                                                                             Q6P256;
                                                                                                                                 Q6P256
            Matches
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                         1 WTFGRNPACDYHLGNISRLSNKHFQIL -- XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GRNPACDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.3%; Score 98.5; DB 2; Length 460; 35.4%; Pred. No. 0.00044; tive 12; Mismatches 29; Indels 1
                                                                                                                                                                                                                                                                                                                                          OrderediocusNames=blr3598;
Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 AA; 50895 MW; C2CC7E01310D367F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          460 AA.
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01-MAR-2003 (TrEMBLrel. 23, Last seq)
01-MAR-2004 (TrEMBLrel. 26, Last annt
ABC transporter ATP-binding protein.
OrderedLocusNames=tll1340;
                                                                                                                                                                                                                                                                Created)
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MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobiaceae; Bradyrhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50006; FHA_DOMAIN; 1.
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InterPro; IPR008984; SMAD_FHA.
                                                                                                                                                                                                                                                                (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
                                                                                                                    94 KNGDVIYV 101
                                                                              59 SQGDEITV 66
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RLTIG 97
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                                                                                                                                                                                                                                                                                                                            Blr3598 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=USDA110;
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Best Local Similarity
                                                                        HSSP; P46014; IMZK.
       Town C.D., Kaul S.,
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Name=F16B3.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WTFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
       Sasamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu
Maiti R., Konning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              GO; GO:0016020 E.membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATPase activity, coupled to transmembrane m.
GO; GO:0000166; F:MTPase activity, coupled to transmembrane m.
InterPro; IPR00169; F:ATPARSE.
InterPro; IPR001899; ABC transporter.
InterPro; IPR001899; ABC transporter.
InterPro; IPR0018994; SMAD FHA.
Pfam; PF000005; ABC trans; I.
Pfam; PF000005; ABC trans; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamotc Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; DNA Res 9:123-130(2002).

-I SIMILARITY: Belongs to the ABC transporter family.

EMBL, AP005373; BAC08892.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%; Score 95; DB 2; Length 1029; 38.2%; Pred. No. 0.003; Live 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SM00240; FHA; 3.
PROSITE; PS00211; ABC TRANSPORTER 1; UNKNOWN 1.
PROSITE; PS008013; ABC TRANSPORTER 2; 1.
PROSITE; PS50006; FHA DOMAIN; 2.
ATP-binding; Complete proteome.
SEQUENCE 1029 AA; 114450 MW; E4E6278B017BD179 CRC64;
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Town C.D., Kaul S.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein F11A12.9 (Fragment).
Name-F11A12.9,
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   567 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
SMART; SM00240; FHA; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 VGDSIRIG 324
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Town C.D., Kaul S.;
Submitted (OCT-2000)
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Best Local Similarity
26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 QGDEITVG 67
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SEQUENCE FROM N.A.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu l
Lin X., Kaul S., Town C.D., Utterback T.R., Barnstead M.B.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO21640, AAF32447.1; -.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000637; A+T_hook.
InterPro; IPR000884; SMAD_FHA.
Pfam; PF02178; AT hook; 2.
Pfam; PF02178; AT hook; 2.
SMART; SM00384; AT hook; 2.
SMART; SM00384; AT hook; 2.
                                                                                  005 00005034, Cinucleus; IEA.

GO; GO:0005634, C:nucleus; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000637; A+T_hook.

InterPro; IPR000533; A+T.

InterPro; IPR00054; SMAD_FHA.

Pfam; PF00178; AT hook; 2.

Pfam; PF00498; FHĀ; 1.

SMART; SM00384; AT hook; 2.
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC068900; AAG12599.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   567 567 567 567 WW; 437AAF6C671CCDAB CRC64;
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SEQUENCE 585 AA; 66387 MW; DBDE57ADAD4ABD42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>::</del>
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Hypothetical protein.
NON TER 567 S67
SEQUENCE 567 AA; 64297 MW; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 EKNSNQLLSQGDEITVG
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13 GRSSSCDVRI-NGNDVSSKHCKLTLTINNNREYLCIKDLSSNGTYLNDEIIGKDSSILLR 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 FGRNPACDYHLGNISR-LSNKHFQILXXXXXLLNDISTNGTWL------NGQKVEKN
                                               4 GRNPACDYHLGNISRLSNKHFQILXX - - - - XXXXLLNDISTNGTWLNGQKVEKNSNQLLS
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PubMed=14656965; DOI=10.1101/gr.1295503;
Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.,
"Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=196600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 27.1%; Score 91; DB 2; Length 374; Local Similarity 35.1%; Pred. No. 0.0034; nes 26; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016809; AA007399.1; -.
InterPro; IPR000253; FHA.
InterPro; IPR00984; SMAD_FHA.
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SEQUENCE 374 AA, 42554 MW; P42608D67A766FE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Uncharacterized conserved protein.
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
21;
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18; Mismatches
                                                                                                                                                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created) 01-WAR-2003 (TrEMBLrel. 23, Last seg 01-OCT-2003 (TrEMBLrel. 25, Last ann Uncharacterized conserved protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
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21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio vulnificus.
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                                                                                                                                                                                     SCDKL 76
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Matches
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A defontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykaeten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lainhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T. "Genome evolution in yeasts.";
19 SLGFKPGSTIRIGRIVRGNEIAIKDAGISTKHLRIVSDSENWIIHDLGSSNGTILNSDTI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50006; FHA_DOMAIN; 1.
PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST;
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 443 AA; 50501 MW; 80B5BACD8BAB9E9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Debaryomyces hansenii CB9767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; CR382139; CAG90972.1; -
GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-cyrobine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.5%; Score 92.5; DB 2; Length 443; 32.3%; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA4770 | IPF9382.3 Candida albicans IPF9382.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000253; FHA.
InterPro; IPR01009; Kinase like.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00498; FHA; 1.
ProDom; PP00069; Pkinase; 1.
                                                                                                                                                                                                                PRT;
                                                                          SDTPVNLSHGDEIKLG 95
                                               EKNSNOLLSOGDEITVG
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SMART; SM00220; S TKC; 1.
SMART; SM00219; TYrKC; 1.
                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      ORFNames=DEHA0G22440g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 430:35-44(2004)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=284592;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CBS767;
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SARRED BRARES BR

10; Gaps

FHA DOMAIN; 1.

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PS50006;
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                                                                                                                                                                                                                                                                               3 FGRNPACDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWL------NGQKVEKN 53
                                                                                                                                                                                                                                        10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSF; G.000524; F.ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:000648; F:protein amino acid phosphorylation; IEA.
InterPro; IPR000253; FHA.
InterPro; IPR00019; Kinase like.
InterPro; IPR008271; Ser Kinase.
InterPro; IPR008271; Ser Kinase.
InterPro; IPR008271; Ser Thr_pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                               27.1%; Score 91; DB 2; Length 434; 35.1%; Pred. No. 0.0039; ive 13; Mismatches 25; Indels
                                                                                                                                                        434 AA; 49606 MW; E5E368A5E1A7CCC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                   Similarity 35.1%; Pred. No. 0.003
26; Conservative 13; Mismatches
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              Genome Res. 13:2577-2587(2003).
EMBL; AP005348; BAC97021.1; -.
INTERPRO; IPR000253; FHA.
InterPro; IPR008984; SMAD_FHA.
PEAM; PF00498; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
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123 DKDVINFGDYEIEV 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7SEK0;
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                   Best Local Similarity
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HSSP; P49137; 1NXK.
                                                                                                                                       Complete proteome. SEQUENCE 434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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  pathogen.";
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Q7SEK0
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R GO; GO:0004674; F:ATP binding; IEA.

R GO; GO:00046713; F:Protein serine/threonine kinase activity; IEA.

R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR001253; F:HA.

R InterPro; IPR00129; Ser thr_pkinase.

R InterPro; IPR00129; Ser thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Prodow; PD000001; Prot_kinase; 1.

R SMART; SM00220; S-TKC; 1.

R SMART; SM00219; TYRC; 1.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB118105; BAC82422.1; -.
HSSP; P22216; IK3Q.
                                                                                                                                                                                                                   Query Match 26.6%; Score 89.5; DB 2; Length 712; Best Local Similarity 32.9%; Pred. No. 0.011; Matches 23; Conservative 14; Mismatches 28; Indels
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PROSITE; PSOUGO7; PROTEIN KINASE ATP; 1.
PROSITE; PSSOULD; PROTEIN KINASE DOM; 1.
ATP-binding; Hypothetical protein; Kinase;
Serinethreonine-protein kinase; Transferase.
SEQUENCE 398 AA; 45996 MW; E9CGADID96A49CB5 CRC64;
PROSITE, PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Hypothetical protein; Kinase;
Serine/threonine-protein kinase; Transferase.
SEQUENCE 712 AA; 79186 MW; A55A2536542B339B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Entamoeba histolytica.
Enkaryota, Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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258 ELQELDEIAV 267
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SMART; SM00240; FHA; 1.
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Q10292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 GRYELCQWCLPDPDRVISGRHALIEKRSGEIIIKDISTNGVFIN-RSVEPLGDEGNYVLS 93
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KEDLINE=21359325; PubMed=11466286;

MEDLINE=21359325; PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Tatusov R.J., Bennett G.N., Koonin B.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838 (2001).

R. BMBL; AB607565; AAK78484.1;

R. HSSP; P46013; 1R21.
                                                                                                                                                                                                                                                                                                                                                                              "Genome analysis of Photobacterium profundum reveals the complexity of
                                                                                                                                                                                                                                                                                                                Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
Cegtaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 87.5; DB 2; Length 436; 36.8%; Pred. No. 0.011; Live 11; Mismatches 27; Indels E
                                                                                                                                                                                Photobacterium profundum (Photobacterium sp. (strain SS9)). Batteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionacea; Photobacterium.
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                   high pressure adaptations.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR318665; CAG19079.1;
InterPro; IPR000253; FHA.
InterPro; IPR0018984; SWAD_FHA.
SPfam; PF00498; FHA; 1.
SWART; SW0040; FHA; 1.
PROSTIE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 AA; 49951 MW; 29ECBDD8C5CEBAC9 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                          (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                           436 AA
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OrderedLocusNames=CAC0504;
                                                                     Created)
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                           PRT;
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InterPro; IPR008984; SMAD_FHA.
Pfam; PF00498; FHA; 1.
                                                                                     05-JUL-2004 (TrEMBLrel. 27, I
05-JUL-2004 (TrEMBLrel. 27, I
Hypothetical protein.
OrderedLocusNames-PBPRA0658;
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                         PRELIMINARY;
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                                                                   05-JUL-2004
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1097L00
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Mood V., Gwilliam R., Radiadram M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., A Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A James K., Jones L., Jones M., Laather S., McDonald S., McLean J., Annes M., Jones M., Laather S., McDonald S., McLean J., Olver K., O'Neil S., Mangall K., Murphy L., Niblett D., Odell C., Olver K., O'Neil S., Barson D., Quail M.A., Rabbinowitsch B., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Askelton J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels B., Reiger M., Schaefer M., Mneller-Ner S., Golden E., Inheat H., Reinhardt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galbert P., Amer S., Jimer R., Modler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Moest J., Moreno S., Armstrong J., Forsburg S.L., America M., Rochet M., Gaillardin C., Fallada V.A., Garzon A., Thode G., Deminguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Revueltia J.L., Moreno S., Armstrong J., Potashkin J., White M., Marker B., Physery B., Barrella G., Nurse P., Warrell G., Nirse P., Warrell G., Nirse P., Warrell G., Nirse P., Warrell G., Nirse P., Warrell G., Nirse P., Warrell G., Nirse P., Warrell G., Nirse P., Warrell G., Mirse P., Warrell G., Nirse P., Warrell G., Nirse P., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G., Warrell G
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                                                                                                                                                                                                                                                                                                                                                  2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Meiosis-specific serine/threonine-protein kinase mek1 (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
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                                                                                                                                                                             Length 159;
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                                                                                                                                                                                                                                                           29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyne M.H., Bryant J.A., Aves S.J.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
PROSITE; PS50006; FHA_DOMAIN; 1.
Complete protecome.
SEQUENCE 159 AA; 17667 MW; F4F44A3D3BF05AA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                         25.9%; Score 87; DB 2; 37.3%; Pred. No. 0.0044;
                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 AA.
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Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                           Query Match
Best Local Similarity 37.3*
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 GDEİKIĞ 151
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opportunistic pathogen.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000001; Prot_kinase; 1.

SWART; SW00240; FHA; 1.

SWART; SW00220; STKc; 1.

PROSITE; PS50001; PRA_BOMIN; 1.

PROSITE; PS50010; PROTEIN KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN KINASE_T; 1.

PROSITE; PS00109; PROTEIN KINASE_T; 1.

PROSITE; PS00109; PROTEIN KINASE_T; 1.

PROPINE | PROTEIN KINASE_T; 1.

PROPINE | PROTEIN KINASE_T; 1.

PROPINE | PROTEIN KINASE_T; 1.

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Pseudomonadaceae; Pseudomonas.
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ATP (By similarity).

Proton acceptor (By similarity)

FOR By similarity).

6D62D79E9A1B45E0 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                          EMBL; 271478; CAA96101.1; -.
EMBL; 298596; CAB11196.1; -.
PIR; T47420; T43420.
HSSP; P49137; 1KWP.
GeneDB_SPombe; SPAC14C4.03; -.
InterPro; IPR01009; Kinase—like,
InterPro; IPR010109; Kinase—like,
InterPro; IPR010109; Kinase—like,
InterPro; IPR010109; Kinase—like,
InterPro; IPR001219; Ser_thr_pkin_AS.
InterPro; IPR008219; Ser_thr_pkin_AS.
InterPro; IPR008294; SWAD_FHA.
Pfam; PF00498; FHA; 1.
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166 174 ATE
281 281 Pro
189 189 ATE
445 AA; 51151 MW; 6
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OrderedLocusNames=PA0081;
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BINDING
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RADEALE-TOCATIONOMS, TANDER TO, OLSUKI T., SUGIYAMM T., ITTE R., TUDWHEG-14702039; DOI=10.1038/ng1285; T., Sugiyama T., ITTE R., WAKAMATEU A., HAYASHI K., SATO H., Nagai K., Kimura K., Makita H., RA WAKAMATEU A., HAYASHI M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Katsuta N., Sato K., Tanikawa M., RA Sugawara M., Ninomiya K., Ishibashi T., Yamashira H., Murakawa M., A Manzaki M., Ninomiya K., Ishibashi T., Yamashira H., Murakawa K., RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., RA Fujimori K., Takahashi-Fujii A., Hara H., Tanase T.-O., RA Imose N., Masshino K., Yuuki H., Oshima A., Sasaki N., Sano S., A Nomiya S., Komiyama H., Ichihara T., Shiohata N., Sano S., A Nokagawa S., Satoh N., Takami A., Takami B., Takamashi W., Watanabe T., Sugiyama A., Takamashi W., Sano S., A Hishigaki H., Watanabe T., Sugiyama A., Takenco M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Takenco M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Takenco M., Kawakami Y., A Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami Y., Yamada K., Fujimori Y., Kumada K., Takinicu H., Tanigami A., Fujiwara T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., Shimizu T., 
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Q96EP1; Q96SL3; Q9NRT4; Q9NT32; Q9NVD5;
29-MAR-2004 (Rel. 43, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Ubiquitin ligase protein CHFR (EC 6.3.2.-) (Checkpoint with forkhead and RNNG finger domains protein).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 25.4%; Score 85.5; DB 2; Length 497; al Similarity 33.3%; Pred. No. 0.024; 23; Conservative 13; Mismatches 30; Indels 3
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Nature 406:959-964 (2000).

EMBL, AB004447; AAG03471.1; -.

EMBL, AB004447; AAG03471.1; -.

InterPro; IPR00053; FHA.

InterPro; IPR008984; SMAD_FHA.

Pfam; PF004408; FHA; 1.

SMART; SM00240; FHA, DOMAIN; 1.

COMPLETE Protecome; Hypothetical protein.

SEQUENCE 497 AA; 53310 MW; AGC63E1D287E7272 CRC64;
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89 QDGETVRLG 97
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Best Local Similarity
Matches 23; Conserv
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TISSUB-Placenta,

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Tetanoberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Tatauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Tatauberg R.L., Teingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

The pkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

The placenon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones S.J.M., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A.;

"Menner A. Schein J.E., Jones M.D., Marra M.A. Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsulwara K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watenabe M., Komatus T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Isogai T., Sugano S., Complete sequencing and characterization of 21,243 full-length human Corn P.G., Summers M.K., Foot F., Virmani A.K., Gazdar A.F., Halazonetis T.D., Bl-Deiry W.S., "Frequent hypermethylation of the 5' CpG island of the mitotic stress checkpoint gene Chfr in colorectal and non-small cell lung cancer."; Carcinogenesis 24:47-51(2003). FUNCTION, AUTOUBLOUITINATION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL FUNCTION, AUTOUBIQUITINATION, AND MUTAGENESIS OF ILE-306 AND TRP-332. PubMed=11807099; DOI=10.1083/jcb.200108016; Kang D., Chen J., Wang J., Fang G.; "The checkpoint protein Chir is a ligase that ubiquitinates Plk1 and inhibits Cdc2 at the G2 to M transition."; Chaturvedi P., Sudakin V., Bobiak M.L., Fisher P.W., Mattern M.R., Jablonski S.A., Hurle M.R., Zhu Y., Yen T.J., Zhou B.-B.; Cifr regulates a mitotic stress pathway through its RING-finger domain with ubiquitin ligase activity."; Cancer Res. 62:1797-1801(2002). ij DISEASE, AND VARIANTS ARG-270; VAL-497 AND MET-580.
PubMed=11948416; DOI=10.1038/sj/onc/1205402;
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"Aberrant hypermethylation of the CHFR prophase checkpoint gene Ottenwaelder B., Obermaier B., Mewes H.-W., Gassenhuber J., Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT VAL-497. and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) PubMed=12538348; DOI=10.1093/carcin/24.1.47; Cell Biol. 156:249-259(2002). SEQUENCE OF 359-664 FROM N.A. human lung cancers."; Oncogene 21:2328-2333(2002). Genet. 36:40-45(2004). PubMed=11912157; Wiemann S.; DISEASE CDNAB."

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X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 14-128.

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 14-128.

Rubmed=12121644; DOI=10.1016/S0969-2126(02)00776-1;

Ry Starvidi E.S., Huyen Y., Loreto I.R., Scolnick D.M., Halazonetis T.D.,

Pavletich N.P., Jeffrey P.D.;

RY Crystal structure of the FHA domain of the Chfr mitotic checkpoint

RY crystal structure of the FHA domain of the Chfr mitotic checkpoint

RY Tructure 10:891-899(2002).

RY crystal structure of the FHA domain of the Chfr mitotic checkpoint

RY Tructure 10:891-899(2002).

RY crystal structure of the FHA domain of the Chfr mitotic checkpoint

RY Tructure 10:891-899(2002).

RY crystal structure of the FHA domain of the Chfr mitotic checkpoint

RY Tructure 10:891-899(2002).

RY Tructure 10:891-899(2002).

RY Tructure 10:891-899(2002).

ATTENDATION: E3 ubiquitin-protein ligase required to transiently

ATTENDATION: E3 ubiquitin-protein ligase required to the along the periphery of the nucleus. Probably promotes the formation of Lyse-

Condense, when the centrosome move apart from each other along the periphery of the nucleus. Probably promotes the formation of Lyse-

Condense, when the centrosome move apart from each other along the periphery of the nucleus. Probably promotes the formation of Lyse-

Condense, when the centrosome move apart from each other along the periphery of the nucleus. Probably promotes the formation of Lyse-

Condense, when the centrosome move apart from each other along the conjugating USC13-Milliane and functions with the specific ubiquitinated for degradation, but are rather involved in signaling expense of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the
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Lys63-linked polyubiquitin chains.";
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Kittas C., Halazonetis T.D., Gorgoulis V.G.;
"Inactivating mutations targeting the chfr mitotic checkpoint gene in
PubMed=12810945; DOI=10.1073/pnas.1337066100;
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Mita H., Tanaka N., Itoh F., Issa J.-P.J., Jair K.-W., Schuebel K.E.,
Imai K., Tokino T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shtivelman E.;
"Promotion of mitosis by activated protein kinase B after DNA damage
"promotion of mitosis by activated protein kinase B after DNA damage
involves polo-like kinase 1 and checkpoint protein CHFR.";
Mol. Cancer Res. 1:959-969(2003).
                                                                                                                                                                                                                            PubMed=14695171;
Satch A., Toyota M., Itoh F., Sasaki Y., Suzuki H., Ogi K.,
Krikuchi T., Mita H., Yamashita T., Kojima T., Kusano M., Fujita M.,
Hosokawa M., Endo T., Tokino T., Imai K.;
"Epigenetic Inactivation of CHFR and sensitivity to microtubule
inhibitors in gastric cancer.";
cancer Res. 63:8606-8613(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erson A.E., Petty E.M.;
"CHPR-associated early G2/M checkpoint defects in breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE, AND VARIANTS NSCLC LEU-166; PRO-202 AND SER-536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION, AND MUTAGENESIS OF THR-39 AND SER-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, INTERACTION WITH UBEZVZ, AND PHOSPHORYLATION
                                                                                                                  tumors.";
                                                                                                                  "Epigenetic inactivation of CHFR in human tumors. Proc. Natl. Acad. Sci. U.S.A. 100:7818-7823(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=3;
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--- PATHWAY: Ubiquitin conjugation; third step.
---- SUBCELLULAR LOCATION: Nuclear.
--- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2;
IsoId=Q96EP1-2; Sequence=VSP_009349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q96EP1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=14694445; DOI=10.1002/mc.10161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human lung cancer.";
Cancer Res. 63:7185-7189(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinog. 39:26-33(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=14638868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=14612512
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                                                                                                                                                                                                       DISEASE
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Last sequence update)

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01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                      strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Chfr;
                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                            97
                                                                                                                                                   1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                          PubMed=14752164; DOI=10.1126/science.1093027; PubMed=14752164; DOI=10.1126/science.1093027; Pendedulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., Sockett R.E., Schuster S.C.; Goesmann A., Meyer F., Sockett R.E., Schuster S.C.; "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from genomic perspective."; Science 303:689-692(2004).

EMBL; BX842647; CAE78455.1; -.
         Note=No experimental confirmation available, TISSUE SPECIFICITY: Ubiquitous. DEVELOPMENTAL STAGE: Weakly expressed in G1 phase, and highly expressed during 8 phase. DOMAIN: The FHA domain may be required to interact with
                                                                                                                                                                                                                                                                                                                             Bdellovibrio bacteriovorus,
Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.3%; Score 85; DB 2; Length 674; 29.9%; Pred. No. 0.039; ive 12; Mismatches 33; Indels
                                                                                              th 25.3%; Score 85; DB 1; Length 664; Similarity 34.8%; Pred. No. 0.038; 23; Conservative 6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 674 AA; 75694 MW; E898524FE1A87766 CRC64;
                                                                                                                                                                                                                                                                                      (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 AA.
                                                                                                                                                                                                                                                         674 AA.
  Isold=Q96EP1-3; Sequence=VSP 009350;
                                                               phosphorylated proteins. -- PTM: Autoubiquitinated in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7UIF2 PRELIMINARY; PRT; Q7UIF2; 01-OCT-2003 (TrEMBLrel. 25, Created)
                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                       PRT;
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InterPro; IPR008994; SMAD FHA.
InterPro; IPR008991; TPR-Tike.
Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 2.
                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=Bd0474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 29.9
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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                                                                                                                                                                                                      98 QTGDVI 103
                                                                                                         Local Similarity
                                                                                                                                                                                 64
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                                                                                                                                                                                 59 SQGDEI
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=959;
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05-JUL-2004
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ID Q7
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4 GRNPACDYHL--GNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
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Q810G13, Q8BAZ9; Q8BMT4;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
ubiquitinn ligase protein CHFR (EC 6.3.2.-) (Checkpoint with forkhead and RING finger domains protein).
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                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                              Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
NCBI_TaxID=117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 AA; 38128 MW; D22946CE39B91677 CRC64;
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294155; CAD77662.1; -.
HSSP; P46014; 1MZK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000253; FHA.
InterPro; IPR000253; FHA.
InterPro; IPR000160; GGDEF.
Pfam; PF00498; FHA; 1.
Pfam; PF00498; FHA; 1.
SMART; SM0267; DUPI; 1.
SMART; SM0267; FHA; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
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PROSITE; PS50887; GGDEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 32.8% nes 22; Conservative
                                                                      OrderedLocusNames=RB12571;
                                                                                                        Rhodopirellula baltica
                                     GGDEF family protein.
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155 GDTVRIG 161
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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degradation of substrates such as PLK, a protein kinase

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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wanning L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Shiraki T., Waki K., Komno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,
Rayazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Myazaki A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Ranalysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.N.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toobilyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Bhakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalak N.,
Butterfield S. S.N., Krzwywinski M.I., Skalak N.,
Butterfield S. S.N., Krzwywinski M.I., Skalak N.,
Butterfield S. S.N., Krzwywinski M.I., Skalak N.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note=No experimental Confirmation available;
Note=No experimental Confirmation available;
DOWAIN: The FHA domain may be required to interact with
phosphorylated proteins (By similarity).
PTM: Autcoubiquitinated in vitro (By similarity).
PTM: Phosphorylated by PKB. Phosphorylation may affect its E3
ligase activity (By similarity).
SIMILARITY: Contains 1 FHA domain.
SIMILARITY: Contains 1 FMG-type zinc finger.
CAUTION: According to some authors it can ubiquitinate and promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: E3 ubiquitin-protein ligase required to transiently arrest cells in early prophase when they are exposed to microtubule poisons. Acts in early prophase before chromosome condense, when the centrosome move apart from each other along the periphery of the nucleus. Probably promotes the formation of Lysebalinked polyubiquitin chains and functions with the specific ubiquitin-conjugating UBEC13-MMS2 (UBE2N-UBE2N2) heterodimer.

Substates that are polyubiquitinated at Lys-63 are usually not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                targeted for degradation, but are rather involved in signaling cellular stress. This suggests that it may be involved in signaling the presence of mitotic stress caused by microtubule poisons (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Ubiquitin conjugation; third step.
SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  involved in mitotic progression. However, as experiments have been done either in vitro or with extracts from Xenopus, there is actually few evidence for a role of CHFR in protein degradation in
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00498; FHA; 1.

Pfam; PF00498; FHA; 1.

SMART; SM00240; PHA; 1.

SMART; SM00240; PHA; 1.

SMART; SM00240; PHA; 1.

PROSITE; PS0006; FHA DOMAIN; 1.

PROSITE; PS00089; ZF_RING_1; 1.

PROSITE; PS00089; ZF_RING_2; 1.

Alternative splicing; Cell cycle; Ligase; Metal-binding; Mitosis; Unclear protein; Phosphorylation; Ubl conjugation, alternative splicing; Cell cycle; Ligase; Metal-binding; Mitosis; DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Biotype gravis / NCTC 13129;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
Cacdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%; Score 84; DB 1; Length 664; 33.3%; Pred. No. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 2).
/FIId=VSP 009351.
Q -> H (in Ref. 1).
G -> C (in Ref. 1).
W, D651BE3E463DEBB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae; Corynebacteriaceae; Corynebacterium
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative signal transduction protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.051;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RING-type.
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                                                                                                                                                                                                                                                                                                                       MGD; MGI:2444898; 5730484M20Rik.
                                                                                                                                                                                                                                                EMBL, AK052473; BAC35008.1; -. EMBL, AK077629; BAC36912.1; -. EMBL; BC049792; AA449792.1; -. HSSP; Q96EP1; 1LGP.
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73871 MW;
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Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SQGDEI 64
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VARSPLIC
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CONFLICT
SEQUENCE
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Q6NHD4
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272 VITVG 276
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                                                                                                             Q8FUH9
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Matches
                                                                 RESULT 35
Q8FUH9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 TAGRHPESDI FLDDVT-VSRRHAEFRRQDGSFEVVDVGSLNGTYVNR---EPRNSEVLSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                             2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-SŢNGTWLNGQKVEKNSNQLLSQGD 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Biocype gravis / NCTC 13129;
MEDLINE=2265543; PubMed=14602910; DOJ=10.1093/nar/gkg874;
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
Whitehead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                      5
                       Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 83.5; DB 2; Length 288; 38.5%; Pred. No. 0.024; ive 10; Mismatches 25; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                  Match 24.9%; Score 83.5; DB 2; Length 143; Local Similarity 31.3%; Pred. No. 0.011; es 21; Conservative 17; Mismatches 24; Indels
Holroyd S., Jagels K., Moule S., Quail M.A.,
sch E., Rutherford K.M., Thomson N.R., Unwin L.,
                                                                                                                                                                                                                                                                                          143 AA; 15264 MW; 7BE05BBB76F8DB1F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 AA.
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                                                                                                         Nucleic Acids Res. 31:6516-6523 (2003).
EMBL; BX248357; CAE49731.1; -.
InterPro; IPRO00253; FHA.
InterPro; IPRO08984; SWAD_FHA.
Pfam; PF00498; FHA; 1.
SWART; SM00240; FHA; 1.
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Nucleic Acids Res. 31:6516-6523(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                              PROSITE; PS50006; FHA DOMAIN; 1.
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InterPro; IPR008984; SMAD_FHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 38.59
Matches 25; Conservative
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                                                                                                                                                                                                                                                                     proteome.
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  Hamlin N.,
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                                                                                                                                                                                                                                                                     Complete
                                                                                                                                                                                                                                                                                             SEQUENCE
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  RA RA RA RA DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT DR RT 
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PubMed=14752164; DOI=10.1126/8cience.1093027;
Rendulic S., Jagtap P., Roshuns A., Eppinger M., Baar C., Lanz C., Sockett R.E., Schuster S.C.;
Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from genomic perspective.";
Science 303:689-692(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bdellovibrio bacteriovorus.
Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.9%; Score 83.5; DB 2; Length 298; ilarity 40.0%; Pred. No. 0.025; Conservative 10; Mismatches 24; Indels
                                                                                                                                                                                                                           Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 13:1572-1579(2003).

EMBL; AP005214; BAC16849.1; -.

HSSP; 946014; IMZK.

InterPro; IPR000353; FHA.

InterPro; IPR008984; SMAD_FHA.

PFam; PF00498; FHA; 1.

SMART; SM00240; FHA, 1.

PROSTIE; PSS0006; FHA, DOMAIN; 1.

Complete proteome; Hypothetical protein.

SEQUENCE 298 AA; 32166 MW; ACAD78F03746781F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                     Last sequence update)
Last annotation update)
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298 AA.
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
Hypothetical protein.
OrderedLocusNames=Bd0472;
                                                      Created)
PRT;
                                                                                  01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                      01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                     Corynebacterium efficiens.
                                                                                                                                                                    OrderedLocusNames=CE0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                                                                          NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
                                                                                                                                                                                                                                                                                   "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AR005274, BAB97440.1;
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INTERPY P46014; IMZK.
INTERPY: IPR000253; FHA.
INTERPY: IPR000253; FHA.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; MSDONG6; FHA DOMAIN; 1.
SCOUPLEE 288 AA; 31317 MM; 1E0E67A6F95AA791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L., Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moockel B., Pfefferle W., Puehler A., Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.";

J. Blotechnol. 104:5-25(2003).

EMBL; BX927148; CAF18615.1; -...
InterPro; IPR000253; FHA.

FIA: Therefore, IPR000894; SMAD_FHA.

FRA: SMO240; FHA; 1.

SMART; SM0240; FHA; 1.

FROSTITE; PS50006; FHA DOMAIN; 1.

FROSTITE; PS50006; FHA DOMAIN; 1.

SMOSTITE; PS50006; FHA DOMAIN; 1.

SEQUENCE 298 AA; 32347 MW; OBF6ASOBA2448BF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
24.3%; Score 81.5; DB 2; Length 288;
Best Local Similarity 38.5%; Pred. No. 0.044;
Matches 25; Conservative 11; Mismatches 24; Indels
                                                                                                                     Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypotherical protein Cg10047.
OrderedLocusAnnes=Cg10047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(0)6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=cg0064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 VITVG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 EITVG 67
                                                                                                                                                                                           NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                            Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fauch A.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                      4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
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Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura B.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.,
                                                                                                                                                                                                           Query Match

24.6%; Score 82.5; DB 2; Length 557;
Best Local Similarity 34.4%; Pred. No. 0.067;
Matches 22; Conservative 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.3%; Score 81.5; DB 2; Length 142; 32.8%; Pred. No. 0.021; ive 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=CB1573;
Corynabacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 13:1572-1579(2003).

EMBL; AP005219; BAC18383.1; -.

HSSP; P46014; IMZK.

InterPro; IPR000828; FHA.

InterPro; IPR008984; SMAD_FHA.

Edm; PF00498; FHA; 1.

SMART; SM00240; FHA DONAIN; 1.

PROSITE; PS50006; FHA DONAIN; 1.

COMPLE profecome; Hypothetical protein.

SEQUENCE 142 AA; 15096 MW; 97C64454E33A1238 CRC64;
                                         InterPro; IPR000253; FHA.
InterPro; IPR000984; SMAD_FHA.
Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
COMPLETE PCCCOMP.
SEQUENCE 557 AA; 60066 MW; C057EB85BF578A20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                   EMBL; BX842647; CAE78453.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                              EITV 66
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82 KLGI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=YS-314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           efficiens.";
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Q8NU92;
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08NU92 1D 08 AC 08

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Gaps

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                                                                                                                               4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-OCT-2004 (Rel. 45, Last annotation update)
17-OCT-2004 (Sel. 46, Last annotation update)
17-OCT-2004 (Sel. 46, Last annotation update)
ORFNames=COIGG.5;
Caenorhabditis elegans.
Caenorhabditis elegans.
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                     5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Query Match 24.3%; Score 81.5; DB 2; Length 298; Best Local Similarity 38.5%; Pred. No. 0.046; Matches 25; Conservative 11; Mismatches 24; Indels !
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MEDLINE=90605613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 24.1%; Score 81; DB 1; Length 952; Local Similarity 41.2%; Pred. No. 0.19; les 14; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 100 FHA.
952 AA; 105274 MW; D9CFB0AB3C685FBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   952 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
-1- SIMILARITY: Contains 1 FHA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mormbase; WBGene00007227; C01G6.5.
WormPep; C01G6.5; CE00867.
InterPro; IPR000253; FHA.
InterPro; IPR000894; SMAD_FHA.
FEam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z35595; CAA84636.1; -. PIR; T18837; T18837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                     283 VITVG 287
                                                                                                                                                                                                                                                                      63 EITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 40
YKIS CAEEL
ID YKIS CAI
AC P46012;
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Search completed: February 24, 2005, 15:23:38 Job time : 128.285 secs